SEQUENCE LISTING

(1)	GENERAL	INFORMATION
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- (i) APPLICANT: JONATHAN EDWARD LIGHTNER JOHN JOSEPH OKULEY
- (ii) TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID DELTA-12 DESATURASES AND RELATED ENZYMES FROM PLANTS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - STREET: 1007 MARKET STREET (B)
 - CITY: WILMINGTON STATE: DELAWARE (C)
 - (D)
 - COUNTRY: U.S.A. (E)
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: MacIntosh
 - (C) OPERATING SYSTEM: MacIntosh 6.0
 - SOFTWARE: Microsoft Word 4.0 (D)
- CURRENT APPLICATION DATA: (vi)
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: U.S. 07/977,339
 - FILING DATE: 17-NOV-1992 (B)
- ATTORNEY/AGENT INFORMATION: (viii)
 - (A) NAME: Siegell, Barbara C.
 - (B) REGISTRATION NUMBER: 30,684
 - (C) REFERENCE/DOCKET NUMBER: BB-1043-B
 - TELECOMMUNICATION INFORMATION: (ix)
 - (A) TELEPHONE: (302) 992-4927 (B) TELEFAX: (302) 892-7949

 - (C) TELEX: 835420

INFORMATION FOR SEQ ID NO:1:

(2)

SEQUENCE CHARACTERISTICS: (i) LENGTH: 1372 base pairs (A) (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear MOLECULE TYPE: (ii) CDNA (iii) HYPOTHETICAL: NO (iv)ANTI-SENSE: NO (vi) ORIGINAL SOURCE: ORGANISM: Arabidopsis thaliana (vii) IMMEDIATE SOURCE: (B) CLONE: p92103 FEATURE: (ix) (A) NAME/KEY: CDS (B) LOCATION: 93..1244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: AGAGAGAGA ATTCTGCGGA GGAGCTTCTT CTTCGTAGGG TGTTCATCGT TATTAACGTT 60 ATCGCCCCTA CGTCAGCTCC ATCTCCAGAA AC ATG GGT GCA GGT GGA AGA ATG 113 Met Gly Ala Gly Gly Arg Met CCG GTT CCT ACT TCT TCC AAG AAA TCG GAA ACC GAC ACA AAG CGT 161 Pro Val Pro Thr Ser Ser Lys Lys Ser Glu Thr Asp Thr Thr Lys Arg 10 GTG CCG TGC GAG AAA CCG CCT TTC TCG GTG GGA GAT CTG AAG AAA GCA 209 Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys Ala ATC CCG CCG CAT TGT TTC AAA CGC TCA ATC CCT CGC TCT TTC TCC TAC 257 Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr CTT ATC AGT GAC ATC ATT ATA GCC TCA TGC TTC TAC TAC GTC GCC ACC 305 Leu Ile Ser Asp Tle Ile Tle Ala Ser Cys Phe Tyr Tyr Val Ala Thr AAT TAC TTC TCT CTC CTC CCT CAG CCT CTC TCT TAC TTG GCT TGG CCA 353 Asn Tyr Phe Ser Leu Leu Pro Gln Pro Leu Ser Tyr Leu Ala Trp Pro CTC TAT TGG GCC TGT CAA GGC TGT GTC CTA ACT GGT ATC TGG GTC ATA 401 Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile 95 100

	TGC Cys							449
	GGT Gly							497
	TAT Tyr							545
	GAA Glu 155							593
	TAC Tyr							641
	GTC Val							689
	TAT Tyr							737
	GAC Asp						GGT Gly	785
	GTC Val 235							833
	ATG Met							881
	GTC Val							929
	GAT Asp							977
	AGA Arg							1025
	CAC His 315							1073

	GCA Ala							ATA Ile									1121
	CAG Gln 345																1169
	GAG Glu																1217
	TAC Tyr							TGAG	CATO	AT G	GTG#	AGAA	A TI	GTC	FACCT		1271
TTCT	CTTC	STC I	GTTI	GTCI	т тт	GTTA	AAGA	AGC	TATO	CTT	CGTI	TTAA	ATA A	TCTI	ATTG	T	1331
CCAT	TTTT	STT G	TGTI	ATGA	C AT	TTTG	GCTG	CTC	ATTA	TGT	T						1372
	(2)	I	NFO	RMAT	ON	FOF	R SE	Q II	NO.	:2:							
			(i)	(. ()	EQUE A) B) D)	LEN TYP	GTH: E:		83 a	STIC amin acid near	o a	cids	3				
		(ii)	MC	LEC.	ULE	TYP	E:	pro	tei	n						
		(xi)	SE	QUE	NCE	DES	CRIE	PTIO	N:	SEC) ID	NO:	2:		•	
	Met 1	,	•												Lys 15	Ser	
	1	Gly	Ala	Gly	Gly 5	Arg	Met	Pro	Val	Pro 10	Thr	Ser	Ser	Lys	_		
	1 Glu	Gly	Ala	Gly Thr 20	Gly 5 Thr	Arg Lys	Met Arg	Pro Val	Val Pro 25	Pro 10 Cys	Thr	Ser	Ser	Lys Pro 30	15	Ser	
	Glu Val	Gly Thr	Ala Asp Asp 35	Gly Thr 20 Leu	Gly 5 Thr Lys	Arg Lys	Met Arg Ala	Pro Val Ile 40	Pro 25	Pro 10 Cys	Thr Glu His	Ser Lys Cys	Ser Pro	Lys Pro 30 Lys	15 Phe	Ser Ser	
	1 Glu Val Ile	Gly Thr Gly Pro 50	Ala Asp Asp 35	Gly Thr 20 Leu Ser	Gly 5 Thr Lys	Arg Lys Lys Ser	Met Arg Ala Tyr 55	Pro Val Ile 40 Leu	Pro 25 Pro	Pro 10 Cys Pro	Thr Glu His	Ser Lys Cys Tle 60	Ser Pro Phe 45	Lys Pro 30 Lys	15 Phe Arg	Ser Ser	
	Glu Val Ile Cys 65	Gly Thr Gly Pro 50 Phe	Ala Asp 35 Arg	Thr 20 Leu Ser	Gly 5 Thr Lys Phe Val	Arg Lys Lys Ser Ala 70	Met Arg Ala Tyr 55	Pro Val Ile 40 Leu Asn	Val Pro 25 Pro Ile	Pro 10 Cys Pro Ser	Thr Glu His Asp Ser 75	Lys Cys Ile 60	Pro Phe 45 Ile	Lys Pro 30 Lys Ile	15 Phe Arg Ala	Ser Ser Pro	
	I Glu Val Ile Cys 65	Gly Thr Gly Pro 50 Phe	Ala Asp Asp 35 Arg	Thr 20 Leu Ser Tyr	Gly 5 Thr Lys Phe Val	Lys Lys Ser Ala 70	Met Arg Ala Tyr 55 Thr	Pro Val Ile 40 Leu Asn	Val Pro 25 Pro Ile Tyr	Pro 10 Cys Pro Ser Phe	Thr Glu His Asp Ser 75 Ala	Lys Cys Ile 60 Leu Cys	Ser Pro Phe 45 Ile Leu	Lys Pro 30 Lys Ile Pro Gly	15 Phe Arg Ala Gln	Ser Ser Pro 80 Val	
	I Glu Val Ile Cys 65 Leu Leu	Gly Thr Gly Pro 50 Phe Ser	Ala Asp Asp 35 Arg Tyr	Thr 20 Leu Ser Tyr Leu	Gly 5 Thr Lys Phe Val Ala 85 Trp	Lys Lys Ser Ala 70 Trp	Met Arg Ala Tyr 55 Thr	Pro Val Ile 40 Leu Asn Leu Ala	Val Pro 25 Pro Ile Tyr Tyr His	Pro 10 Cys Pro Ser Phe	Thr Glu His Asp Ser 75 Ala	Lys Cys Ile 60 Leu Cys	Ser Pro Phe 45 Ile Leu Gln His	Lys Pro 30 Lys Ile Pro Gly His	Phe Arg Ala Gln Cys 95	Ser Ser Pro 80 Val	

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp 275 280 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu 295 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

			(111	.,	III O	* * * * *	ı ÇA.	٠ بــ	NO								
			(iv	7) A	ITN.	-SEN	SE:	NC)								
			(vi		RIG: (A)		SO SANI		E: Br	ass:	ica	nap	us				
			(vii		MMEI (B)					1651)						
			(i;	· (EATI (A) (B)	NAM	Œ/K		CD 99	-	250						
			(xi	L) S	EQU	ENCE	DE	SCRI	PTI	ON:	SE	Q II	O NC	:3:			
GAG	AGGA	GAC	AGAG	ACAG	AG A	GAGA	GTTG	A GA	GAGC	TCTC	GTA	GGTT	ATC	GTAT	TAACGT	r	60
AAT	CTTC.	AAT	cccc	CCTA	CG T	CAGC	CAGC	T CA	AGAA					GT G ly G			113
			GTG Val														161
			CCC Pro 25	Cys											AAG Lys		209
			CCA Pro														257
TCC Ser	CAC His 55	CTC Leu	ATC Ile	TGG Trp	GAC Asp	ATC Ile 60	ATC Ile	ATA Ile	GCC Ala	TCC Ser	TGC Cys 65	TTC Phe	TAC Tyr	TAC Tyr	GTC Val		305
			TAC Tyr												GCC Ala 85		353
TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAG Gln	GGC Gly	TGC Cys 95	GTC Val	CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp		401
			CAC His 105														बिक्ष
CTG Leu	GAC Asp	GAC Asp 120	ACC Thr	GTC Val	GGC Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser	TTC Phe	CTC Leu 130	CTC Leu	GTC Val	CCT Pro		497

TAC Tyr	TTC Phe 135	Ser	TGG Trp	AA G Lys	TAC Tyr	AGT Ser 140	CAT His	CGA Arg	. CGC Arg	CAC	CAT His 145	Ser	AAC Asn	ACT Thr	GGC Gly	545
			AGA Arg								Arg					593
AGT Ser	GGT Gly	ACG Thr	GCA Ala	AGT Ser 170	ACC Thr	TCA Ser	ACA Thr	ACC Thr	TTT Phe 175	GGA Gly	CGC	ACC Thr	GTG Val	ATG Met 180	TTA Leu	641
			TTC Phe 185													689
			CCT Pro													737
			TAC Tyr													785
GCT Ala 230	GGC Gly	ATC Ile	CTC Leu	GCC Ala	GTC Val 235	TGC Cys	TAC Tyr	GGT Gly	CTG Leu	CTA Leu 240	CCG Pro	TAC Tyr	GCT Ala	GCT Ala	GTC Val 245	833
CAA Gln	GGA Gly	GTT Val	GCC Ala	TCG Ser 250	ATG Met	GTC Val	TGC Cys	TTC Phe	CTA Leu 255	CGA Arg	GTT Val	CCT Pro	CTT Leu	CTG Leu 260	ATT Ile	881
			TTC Phe 265													929
			CAC His													977
			GTT Val													1025
AAT Asn 310	ATC Ile	ACG Thr	GAC Asp	ACG Thr	CAC His 315	GAG Glu	GCG Ala	CAT His	CAC His	CTG Leu 320	TTC Phe	TCG Ser	ACC Thr	ATG Met	CCG Pro 325	1073
CAT Hiq	TAT Tyr	CAT His	GCG Ala	ATG Met 330	GAA Glu	GCT Ala	ACG Thr	AAG Lys	GCG Ala 335	ATA Ile	AA G Lys	CCG Pro	ATA Ile	CTG Leu 340	GGA Gly	1121
GAG Glu	TAT Tyr	TAT Tyr	CAG Gln 345	TTC Phe	GAT Asp	GGG Gly	ACG Thr	CCG Pro 350	GTG Val	GTT Val	AAG Lys	GCG Ala	ATG Met 355	TGG Trp	AGG Arg	1169

	GCG Ala																1217
	GGT Gly 375									TGAA	(GCAA	AG A	AGAZ	ACTO	GA		1267
ACCI	TTCI	CT T	CTAT	CAAT	T GT	CTTT	GTTI	' AAG	AAGC	TAT	GTTI	CTGI	TT C	AATA	ATCT	T.	1327
AATI	ATCC	AT T	TTGT	TGTG	т тт	TCTG	ACAT	TTT	GGCI	'AAA	ATTA	TGTG	AT G	TTGG	SAAGT	T	1387
AGTO	TCT																1394
	(2)	I	NFOF	RMAT	ION	FOR	SE	Q II) NO	:4:							
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein 																
		(ii)	MOL	ECUI	LE I	YPE	: F	prot	ein							
		(:	xi)	SEQ	UEN	CE D	ESC	RIPT	rion	: 3	SEQ	ID :	NO : 4	l :			
	Met 1	Gly	Ala	Gly	Gly 5	Arg	Met	Gln	Val	Ser 10	Pro	Pro	Ser	Lys	Lys 15	Ser	
	Glu	Thr	Asp	Asn 20	Ile	Lys	Arg	Val	Pro 25	Cys	Glu	Thr	Pro	Pro 30	Phe	Thr	
	Val	Gly	Glu 35	Leu	Lys	Lys	Ala	Ile 40	Pro	Pro	His	Cys	Phe 45	Lys	Arg	Ser	
	Ile	Pro 50	Arg	Ser	Phe	Ser	His 55	Leu	Ile	Trp	Asp	Ile 60	Ile	Ile	Ala	Ser	
	Cys 65	Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	Pro	Asn	Pro 80	
	Leu	Ser	Tyr	Phe	Ala 85	Trp	Pro	Leu	Tyr	Trp 90	Ala	Суз	Gln	Gly	С у з 95	Val	
	Leu	Thr	Gly	Val 100	Trp	Val	Ile	Ala	His 105	Glu	Суз	Gly	His	Ala 110	Ala	Phe	
	Ser	Asp	Tyr 115	Gln	Trp	Leu	Asp	Asp 120	Thr	Val	Gly	Leu	Ile 125	Phe	His	Ser	
	Phe	Leu 130	Leu	Val	Pro	Tyr	Phe 135	Ser	Trp	Lys	Tyr	Ser 140	His	Arg	Arg	His	
	His 145	Ser	Asn	Thr	Gly	Ser 150	Leu	Glu	Arg	Asp	Glu 155	Val	Phe	Val	Pro	Arg 160	
	Arg	Ser	Gln	Thr	Ser 165	Ser	Gly	Thr	Ala	Ser 170	Thr	Ser	Thr	Thr	Phe 175	Gly	

 Arg
 Thr
 Val
 Met
 Leu
 Thr
 Val
 Gln
 Phe
 Thr
 Leu
 Gly
 Trp
 Pro
 Leu
 Trp
 Pro
 Trp
 Pro
 Ash
 Cys
 Pro
 Pro
 Ash
 Ala
 Pro
 Ile
 Trp
 Ash
 Asp
 Asp
 Ala
 Pro
 Ile
 Trp
 Ash
 Asp
 Asp
 Ala
 Pro
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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Glycine max

(vii) IMMEDIATE SOURCE:

			· · ·	-,	(B)	CI			SF2	-16	5K						
			(i)	<)	FEA: (A) (B)	NA	: ME/: CAT			DS 08.	.124	7					
			ix)	L)	SEQ	JENC	E DI	ESCF	RIPT	ION:	: S	EQ I	ID N	0:5	:		
CCA	TATA	CTA	ATAT	TTGC	TT G	TATT	GATA	G CC	CCTC	CGTT	ccc	AAGA	GTA	TAAA	ACTGCA	6	60
TCG	AATA	ATA	CAAG	CCAC	TA G	GCAT	GGGT	С ТА	GCAA	AGGA	AAC	AACA		Gly	GGT Gly	. 11	. 6
AGA Arg	GGT Gly 5	Arg	GTG Val	GCC Ala	AAA Lys	GTG Val 10	Glu	GTT Val	CAA Gln	GGG Gly	AAG Lys 15	Lys	CCT Pro	CTC Leu	TCA Ser	16	4
AGG Arg 20	GTT Val	CCA Pro	AAC Asn	ACA Thr	AAG Lys 25	CCA Pro	CCA Pro	TTC Phe	ACT Thr	GTT Val 30	GGC Gly	CAA Gln	CTC Leu	AAG Lys	AAA Lys 35	21	.2
GCA Ala	ATT	CCA Pro	CCA Pro	CAC His 40	TGC Cys	TTT Phe	CAG Gln	CGC A rg	TCC Ser 45	CTC Leu	CTC Leu	ACT Thr	TCA Ser	TTC Phe 50	TCC Ser	26	O
					CTT Leu										ACC Thr ,	30	8
ACC Thr	TAC Tyr	TTC Phe 70	CAC	CTC Leu	CTT Leu	CCT Pro	CAA Gln 75	CCC Pro	TTT Phe	TCC Ser	CTC Leu	ATT Ile 80	GCA Ala	TGG Trp	CCA Pro	35	6
ATC Ile	TAT Tyr 85	TGG Trp	GTT Val	CTC Leu	CAA Gln	GGT Gly 90	TGC Cys	CTT Leu	CTC Leu	ACT Thr	GGT Gly 95	GTG Val	TGG Trp	GTG Val	ATT Ile	40	4
GCT Ala 100	CAC His	GAG Glu	TGT Cys	GGT Gly	CAC His 105	CAT His	GCC Ala	TTC Phe	AGC Ser	AAG Lys 110	TAC Tyr	CAA Gln	TGG Trp	GTT Val	GAT Asp 115	45	2
					ACC Thr										TTC Phe	50	С
TCA Ser	TGG Trp	AAA Lys	ATA Ile 135	AGC Ser	CAT His	CGC Arg	CGC Arg	CAT His 140	CAC His	TCC Ser	AAC Asn	ACA Thr	GGT Gly 145	TCC Ser	CTT Leu	54	8
GAC Asp	CGT Arg	GAT. Asp 150	GAA Glu	GTG Val	TTT Phe	GTC Val	CCA Pro 155	AAA Lys	CCA Pro	AAA Lys	TCC Ser	AAA Lys 160	GTT Val	GCA Ala	TGG Trp	59	6

TTT Phe	TCC Ser 165	Lys	TAC Tyr	TTA Leu	AAC Asn	AAC Asn 170	CCT Pro	CTA Leu	GGA Gly	AGG Arg	GCT Ala 175	GTT Val	TCT Ser	CTT Leu	CTC Leu	644
						TGG Trp										692
						TTT Phe										740
						AGG Arg										788
						TCT Ser										836
						GTT Val 250										884
						ACA Thr										932
						GAA Glu										980
						GGG Gly										1028
ACT Thr	GAT Asp	ACT Thr 310	CAT His	GTG Val	GCT Ala	CAC His	CAT His 315	CTC Leu	TTC Phe	TCT Ser	ACA Thr	ATG Met 320	CCA Pro	CAT His	TAC Tyr	1076
						AAT Asn 330										1124
						CCA Pro										1172
						GAG Glu										1220
						AAG Lys		TGAT 380	'GGAG	CA A	CCAA	\TGGG	GC CA	TAGI	'GGGA	1274
GTTA	TGGA	AG T	TTTG	TCAT	G TA	TTAG	TACA	TAA	TTAG	TAG	AATG	TTAT	'AA A	TAAG	TGGA	r 1334

TTGCCGC	GTA A	ATGA	CTTTC	GT GT	rgtai	TGTC	AA.	ACAGO	CTTG	TTG	CGAT	CAT	GTT	ATAAT	rG
TAAAAAT	AAT 1	CTG	STATI	ra at	TAC	ATGTO	GA2	AAGTO	STTC	TGC	TAT	AGC 2	TTC	rgcci	ΓA
AAAAAA	A														
(2)]	NFO	RMAI	CION	FOR	R SE	Q II	D NC	:6:						
		(i)	SE((A) (B) (D)	L. T	CE (ENGT YPE: OPOI	TH:	379 mino		ino id	S: aci	.ds				
	((ii)	MOI	LECU	LE :	TYPE	:	prot	ein						-
	((xi)	SEC	QUEN	CE I	DESC	RIP'	TION	T:	SEQ	ID	NO:	6 :		
_	Gly	Gly	Arg	Gly 5	Arg	Val	Ala	Lys	Val 10		Val	Gln	Gly	Lys 15	Lys
Pro	Leu	Ser	Arg 20	Val	Pro	Asn	Thr	Lys 25	Pro	Pro	Phe	Thr	Val 30	Gly	Gln
Leu	Lys	Lys 35	Ala	Ile	Pro	Pro	His 40	Суз	Phe	Gln	Arg	Ser 45	Leu	Leu	Thr
Ser	Phe 50		Tyr	Val	Val	Tyr 55	ДЗP	Leu	Ser	Phe	Ala 60	Phe	Ile	Phe	Tyr
Ile 65	Ala	Thr	Thr	Tyr	Phe 70	His	Leu	Leu	Pro	Gln 75	Pro	Phe	Ser	Leu	Ile 80
Ala	Trp	Pro	Ile	Туг 85		Val	Leu	Gln	Gly 90	Суз	Leu	Leu	Thr	Gly 95	Val
Trp	Val	Ile	Ala 100	His	Glu	Cys	Gly	His 105	His	Ala	Phe	Ser	Lys 110	Tyr	Gln
Trp	Val	Asp 115	Asp	Val	Val	Gly	Leu 120	Thr	Leu	His	Ser	Thr 125	Leu	Leu	Val
Pro	Tyr 130	Phe	Ser	Trp	Lys	Ile 135			_	Arg		His	Ser	Asn	Thr
Gly 1 4 5	Ser	Leu	Asp	Arg	Asp 150	Glu	Val	Phe	Val	Pro 155	Lys	Pro	Lys	Ser	Lys 160
Val	Ala	Trp	Phe	Ser 165	Lys	Tyr	Leu	Asn	Asn 170	Pro	Leu	Gly	Arg	Ala 175	Val
Ser	Leu	Leu	Val 180	Thr	Leu	Thr	Ile	Gly 185	Trp	Pro	Met	Tyr	Leu 190	Ala	Phe
Asn	Val	Ser 195	Gly	Arg	Pro	Tyr	Asp 200	Ser	Phe	Ala	Ser	His 205	Tyr	His	Pro

Tyr Ala Pro Ile Tyr Ser Asn Arg Glu Arg Leu Leu Ile Tyr Val Ser 210 215 220

Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val Ala Thr 225 230 235 240

Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro Leu Leu 245 250 255

Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Gln His Thr His 260 265 270

Phe Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly 275 280 285

Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe 290 295 300

His His Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met 305 310 315 320

Pro His Tyr His Ala Met Glu Ala Thr Asn Ala Ile Lys Pro Ile Leu 325 330 335

Gly Glu Tyr Tyr Gln Phe Asp Asp Thr Pro Phe Tyr Lys Ala Leu Trp 340 345 350

Arg Glu Ala Arg Glu Cys Leu Tyr Val Glu Pro Asp Glu Gly Thr Ser 355 360 365

Glu Lys Gly Val Tyr Trp Tyr Arg Asn Lys Tyr 370 375

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1790 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Zea mays
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: pFad2#1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 165..1328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGG	CCTC	TCC	CCTC	CCTC	CT C	CCTG	CAAA	T CC	TGCA	GACA	CCA	.CCGC	TCG	TTTT	TCTCTC	60
CGG	GACA	GGA	GAAA	AGGG	GA G	AGAG	AGGT	g ag	GCGC	ggtg	TCC	GCCC	GAT	CTGC	TCTGCC	120
CCG	ACGC.	AGC	TGTT.	acga	CC T	ССТС	AGTC'	T CA	GTCA	ggag	CAA	Me			C GGC a Gly	176
							CGG Arg									224
							CAG Gln									272
							AAG Lys									320
							TCG Ser 60									368
							GCG Ala									416
							TGG Trp									464
							GTC Val									512
							CTG Leu									560
							TAC Tyr 140									608
							TCC Ser									656
CCC Pro 165	AAG Lys	AAG Lys.	AAG Lys	GAG Glu	GCG Ala 170	CTG Leu	CCG Pro	TGG Trp	TAC Tyr	ACC Thr 175	CCG Pro	TAC Tyr	GTG Val	TAC Tyr	AAC Asn 180	704

AAC Asn	Pro	GTO Val	GGC Gly	CGC Arg 185	y val	G GTG	CAC His	C ATO	C GT(e Val	L Val	G CAC	G CTO	C ACC	CTC Let	G GGG Gly	752	?
TGG Trp	CCG Pro	CTC Leu	TAC Tyr 200	Let	G GCC	ACC Thr	AAC Asr	GC0 Ala 205	a Ser	GG(G CGG 7 Arg	Fro	TAC Tyr 210	Pro	G CGC	800	1
TTC Phe	GCC Ala	TGC Cys 215	HIS	TTC Phe	GAC Asp	CCC Pro	TAC Tyr 220	: Gl	C CCC	ATC	TAC Tyr	AAC Asn 225	qeA ı	CGC Arc	G GAG g Glu	848	!
CGC A rg	GCC Ala 230	Gin	ATC	TTC Phe	GTC Val	TCG Ser 235	GAC Asp	GCC Ala	GGC Gly	GTC Val	GTG Val 240	Ala	GTG Val	GCG	TTC Phe	896	
GGG Gly 245	CTG Leu	TAC Tyr	AAG Lys	CTG Leu	GCG Ala 250	GCG Ala	GCG Ala	TTC	GGG Gly	GTC Val 255	Trp	TGG Trp	GTG Val	GTG Val	CGC Arg 260	944	
GTG Val	TAC Tyr	GCC Ala	GTG Val	CCG Pro 265	CTG Leu	CTG Leu	ATC Ile	GTG Val	AAC Asn 270	GCG Ala	TGG Trp	CTG Leu	GTG Val	CTC Leu 275	ATC Ile	992	
ACC Thr	TAC Tyr	CTG Leu	CAG Gln 280	CAC His	ACC Thr	CAC His	CCG Pro	TCG Ser 285	CTC Leu	CCC Pro	CAC His	TAC Tyr	GAC Asp 290	TCG Ser	AGC Ser	1040	
GAG Glu	TGG Trp	GAC Asp 295	TGG Trp	CTG Leu	CGC Arg	GGC Gly	GCG Ala 300	CTG Leu	GCC Ala	ACC Thr	ATG Met	GAC Asp 305	CGC Arg	GAC Asp	TAC Tyr	1088	
GIY	ATC Ile 310	CTC Leu	AAC Asn	CGC Arg	GTG Val	TTC Phe 315	CAC His	AAC Asn	ATC Ile	ACG Thr	GAC Asp 320	ACG Thr	CAC His	GTC Val	GCG Ala	1136	
CAC His 325	CAC His	CTC Leu	TTC Phe	TCC Ser	ACC Thr 330	ATG Met	CCG Pro	CAC His	TAC Tyr	CAC His 335	GCC Ala	ATG Met	GAG Glu	GCC Ala	ACC Thr 340	1184	
AAG (GCG Ala	ATC Ile	Arg	CCC Pro 345	ATC Ile	CTC Leu	GGC Gly	GAC Asp	TAC Tyr 350	TAC Tyr	CAC His	TTC Phe	qzA	CCG Pro 355	ACC Thr	1232	
CCT (GTC /	Ala	AAG (Lys)	GCG Ala	ACC Thr	TGG (Arg	GAG Glu 365	GCC Ala	GGG Gly	GAA Glu	Cys	ATC Ile 370	TAC Tyr	GTC Val	1280	
GAG (Glu F	LO (GAG (Glu / 375	GAC (CGC . Arg :	AAG (GIY V	GTC Val 380	TTC Phe	TGG	TAC .	Asn :	AAG Lys 385	AAG ' Lys 1	TTC Phe	TAGCCGC	GGC 13:	35
CGCTC	GCA	GA GO	CTGA	GGAC	G CT	ACCGI	AGG	AAT	GGGA	GCA (GAAA	CCAG	GA GO	GAGG	AGACG	1395	
GTACT	CGC	cc ca	AAAG:	CTC	C GT	CAACO	TAT	CTA	ATCG:	TTA (GTCG:	rcag:	rc T	TTA	GACGG	1455	
GAAGA	GAG	AT C	ATTTO	GGC	A CAC	GAGAC	GAA	GGC'	TTAC	rgc i	AGTG	CCAT	CG C	raga	GCTGC	1515	

								143							
CATCAAG	rac A	AAGTA	GGCA.	A AI	TCGI	CAAC	TTA	GTGT	GTC	CCAT	GTTG	err 1	TTCI	TAGI	'C
GTCCGCT	SCT (STAGG	CTTT	C CG	GCGG	CGGT	CGT	TTGT	GTG	GTTG	GCAT	CC G	STGGC	CATG	C
CTGTGCG	rgc e	TGGC	CGCGG	с тт	GTCG	TGTG	CGT	CTGT	CGT	CGCG	TTGG	icg 1	CGTC	TCTT	'C
GTGCTCC	CCG 1	GTGT	TGTT	3 TA	AAAC	AAGA	AGA	TGTT	TTC	TGGT	GTCT	TT G	GCGG	AATA	A
CAGATCG	rcc e	SAACG	AAAA	A AA	AAAA	AAAA	AAA	AA							
(2)	(2) INFORMATION FOR SEQ ID NO:8:														
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 387 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein														
	(ii)	MOL	ECU:	LE I	YPE	: E	prot	ein						
	(xi)	SEQ	UEN	CE I	DESC:	RIPT	rion	: :	SEQ	ID 1	NO : 8	3:		
Met 1		Ala	Gly	Gly 5	Arg	Met	Thr	Glu	Lys 10	Glu	Arg	Glu	Lys	Gln 15	Glu
Gln	Leu	Ala	Arg 20	Ala	Thr	Gly	Gly	Ala 25	Ala	Met	Gln	Arg	Ser 30	Pro	Val
Glu	Lys	Pro 35	Pro	Phe	Thr	Leu	Gly 40	Gln	Ile	Lys	Lys	Ala 45	Ile	Pro	Pro
His	Суз 50	Phe	Glu	Arg	Ser	Val 55	Leu	Lys	Ser	Phe	Ser 60	Tyr	Val	Val	His
Asp 65		Val	Ile	Ala	Ala 70	Ala	Leu	Leu	Tyr	Phe 75	Ala	Leu	Ala	Ile	Ile 80
Pro	Ala	Leu	Pro	Ser 85	Pro	Leu	Arg	Tyr	Ala 90	Ala	Trp	Pro	Leu	Tyr 95	Trp
Ile	Ala	Gln	Gly 100	Суз	Val	Суз	Thr	Gly 105	Val	Trp	Val	Ile	Ala 110	His	Glu

Cys Gly His His Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp

Glu Val Phe Val Pro Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His 340 345 350

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu 355 360 365

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn 370 375 380

Lys Lys Phe 385

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Ricinus communis

		(v	ii)	IMM (B)	EDI <i>F</i> CI			RCE:	-1C						
		(ix)	FEA (A) (B)		ME/	KEY:		DS 6	73					
		(xi)	SEQ	UENC	E D	ESCI	RIPT	ION	: s	EQ	ID N	10:9	:	
TGG G Trp V 1	STG A	TG G et A	CG CA la Hi	T GAT s Ası 5	TGT Cys	GGG Gly	CAC His	CAT His	Ala	TTC Phe	AGT Ser	GAC Asp	TAT	Gln	48
TTG C Leu L	TT G	SP A	AT GT BP Va 20	A GTT l Val	GGT Gly	CTT Leu	ATC Ile 25	Leu	CAC His	TCC	TGT Cys	CTC Leu 30	Leu	GTC Val	96
CCT T Pro T	yr Pi	rr ro ne Se 35	CA TG	G AAA p Lys	CAC His	AGC Ser 40	CAT His	CGC	CGA Arg	CAT	CAT His 45	TCC Ser	AAC Asn	ACA Thr	144
GGG TG	CC C1 er Le 50	rG Gz eu Gl	A CG	TAD E qea q	GAA Glu 55	GTG Val	TTT Phe	GTT Val	CCC Pro	AAG Lys 60	AAG Lys	AAA Lys	TCT Ser	AGT Ser	192
ATC CO Ile A	GT TO	G TA	T TC	C AAA Lys 70	Tyr	CTC Leu	AAC Asn	AAC Asn	CCT Pro 75	CCA Pro	GGT Gly	CGT Arg	ATC Ile	ATG Met 80	240
ACA A'	TT GO le Al	C GT .a Va	C AC	. Leu	TCA Ser	CTT Leu	GGC Gly	TGG Trp 90	CCT Pro	CTG Leu	TAC Tyr	CTA Leu	GCA Ala 95	TTC Phe	. 288
AAT G Asn V	TT TC al Se	A GG r Gl 10	y Arg	G CCA J Pro	TAT Tyr	GAT Asp	CGG Arg 105	TTC Phe	GCC Ala	TGC EY3	CAC His	TAT Tyr 110	GAC Asp	CCA Pro	336
TAT GO	GC CC Ly Pr 11	o Il	C TAC	AAT Asn	GAT Asp	CGC Arg 120	GAG Glu	CGA Arg	ATC Ile	GAG Glu	ATA Ile 125	TTC Phe	ATA Ile	TCA Ser	384
GAT GO Asp Al	la Gl	T GT y Va	T CTI l Leu	GCT Ala	GTC Val 135	ACT Thr	TTT Phe	GGT Gly	CTC Leu	TAC Tyr 140	CAA Gln	CTT Leu	GCT Ala	ATA Ile	432
GCG AA Ala Ly 145	G GG	G CT y Le	T GCT u Ala	TGG Trp 150	GTT Val	GTC Val	TGT Cys	GTA Val	TAT Tyr 155	GGA Gly	GTG Val	CCA Pro	TTG Leu	TTG Leu 160	480
GTG GT Val Va	G AA	T TC. n Se	A TTC r Phe 165	Leu	GTT Val	CTG Leu	ATC Ile	ACA Thr 170	TTT Phe	CTG Leu	CAG Gln	CAT His	ACT Thr 175	CAC His	528
CCT GC	A TTO	G CC. u Pro 18	o His	TAT Tyr	GAT Asp	TCG Ser	TCG Ser 185	GAG Glu	TGG Trp	GAC Asp	TGG Trp	CTA Leu 190	AGA Arg	GGA Gly	576

GCT Ala	CTA Leu	GCA Ala 195	ACT Thr	GTT Val	GAC Asp	AGA Arg	GAT Asp 200	TAC Tyr	GGG Gly	ATC Ile	TTG Leu	AAC Asn 205	AAG Lys	GTG Val	TTC Phe		624
CAT His	AAC Asn 210	ATA Ile	ACG Thr	GAC Asp	ACT Thr	CAA Gln 215	GTA Val	GCT Ala	CAC His	CAC His	CTT Leu 220	TTC Phe	ACC Thr	ATG Met	CCC Pro	С	673
	(2)	I	NFO	RMAT	CION	FO	R SI	EQ I	D N	0:10):						
			(i)	SEÇ (A (B (D) I	JENG TYPE	TH:	amir	24 a 10 a	min		cids					
		(ii)	MOL	ECU	LE '	TYPE	Ξ:	pro	ceir	1						
		(xi)	SEÇ	UEN	CE 1	DESC	CRIP	TIOI	N:	SEQ	ID	NO:	10:			
	Trp 1	Val	Met	Ala	His 5	Asp	Cys	Gly	His	His 10	Ala	Phe	Ser	Asp	Tyr 15	Gln	
	Leu	Leu	Asp	Asp 20	Val	Val	Gly	Leu	Ile 25	Leu	His	Ser	Cys	Leu 30	Leu	Val	
	Pro	Tyr	Phe 35	Ser	Trp	Lys	His	Ser 40	His	Arg	Arg	His	His 45	Ser	Asn	Thr	
	Gly	Ser 50	Leu	Glu	Arg	Asp	Glu 55	Val	Phe	Val	Pro	Lys 60	Lys	Lys	Ser	Ser	
	Ile 65	Arg	Trp	Tyr	Ser	Lys 70	Tyr	Leu	Asn	Asn	Pro 75	Pro	Gly	Arg	Ile	Met 80	
	Thr	Ile	Ala	Val	Thr 85	Leu	Ser	Leu	Gly	Trp 90	Pro	Leu	Tyr	Leu	Ala 95	Phe	
	Asn	Val	Ser	Gly 100	Arg	Pro	Tyr	Asp	Arg 105	Phe	Ala	Cys	His	Tyr 110	Asp	Pro	
	Tyr	Gly	Pro 115	Ile	Tyr	Asn	Asp	Arg 120	Glu	Arg	Ile	Glu	Ile 125	Phe	Ile	Ser	
	Asp	Ala 130	Gly	Val	Leu	Ala	Val 135	Thr	Phe	Gly	Leu	Tyr 140	Gln	Leu	Ala	Ile	
	Ala 145	Lys	Gly	Leu	Ala	Trp 150	Val	Val	Cys	Val	Tyr 155	Gly	Val	Pro	Leu	Leu 160	
	Val	Val	Asn	Ser	Phe 165	Leu	Val	Leu	Ile	Thr 170	Phe	Leu	Gln	His	Thr 175	His	
	Pro	Ala	Leu	Pro 180	His	Tyr	Asp	Ser	Ser 195	Glu	Trp	Asp	Trp	Leu 190	Arg	Gly	
	Ala	Leu	Ala 195	Thr	Val	Asp	Arg	Asp 200	Tyr	Gly	Ile	Leu	Asn 205	Lys	Val	Phe	

His Asn Ile 1 210	Thr Asp Thr Gln 1 215	/al Ala His His	Leu Phe Thr Met 220	Pro
(2) INFORM	ATION FOR SEQ	ID NO:11:		
(i)	SEQUENCE CHAI (A) LENGTH: (B) TYPE: n (C) STRANDED (D) TOPOLOGY	1369 base paucleic acid NESS: double		
(ii)	MOLECULE TYPE	: cDNA		
(iii)	HYPOTHETICAL:	NO		
(iv)	ANTI-SENSE:	NO		
(vi)	ORIGINAL SOUR (A) ORGANISM		ommunis	
(vii)	IMMEDIATE SOU (B) CLONE:]	RCE: pRF197c-42		
(ix)	FEATURE: (A) NAME/KEY (B) LOCATION			
(xi)	SEQUENCE DESC	RIPTION: SEC) ID NO:11:	
CGGCCGGGAT TCCGGTT	TTC ACACTAATTT GO	CAAAAAATG CATGA	TTTCA CCTCAAATCA	60
AACACCACAC CTTATAAC	CTT AGTCTTAAGA GA	AGAGAGAGA GAGGA	GACAT TTCTCTTCTC	120
TGAGATGAGC ACTTCTCT	TC CAGACATCGA AC	SCCTCAGGA AAGTG	CTTGA GAAGAGCTTG	180
AGA ATG GGA GGT GGT Met Gly Gly Gly 1	GGT CGC ATG TCT Gly Arg Met Ser 5	TACT GTC ATA AS Thr Val Ile II	TC AGC AAC AAC le Ser Asn Asn 15	228
AGT GAG AAG AAA GGA Ser Glu Lys Lys Gly 20	Gly Ser Ser His	CTG GAG CGA GG Leu Glu Arg Al 25	CG CCG CAC ACG la Pro His Thr 30	276
AAG CCT CCT TAC ACA Lys Pro Pro Tyr Thr 35	CTT GGT AAC CTC Leu Gly Asn Leu 40	Lys Arg Ala Il	PC CCA CCC CAT Le Pro Pro His 45	324
TGC TTT GAA CGC TCT Cys Phe Glu Arg Ser 50	TTT GTG CGC TCA Phe Val Arg Ser 55	Phe Ser Asn Ph	TT GCC TAT AAT ne Ala Tyr Asn 50	372
TTC TGC TTA AGT TTT Phe Cys Leu Ser Phe 65	CTT TCC TAC TCG Leu Ser Tyr Ser 70	ATC GCC ACC AA Ile Ala Thr As	C TTC TTC CCT	420

															CTC Leu 95	468
					Leu							GGC Gly				516
				Phe					Leu			GAC Asp			GGC Gly	564
CTA Leu	ATT Ile	GTC Val 130	CAT	TCT Ser	GCA Ala	CTT Leu	CTG Leu 135	GTT Val	CCA Pro	TAT Tyr	TTT Phe	TCA Ser 140	TGG Trp	AAA Lys	TAT Tyr	612
AGC Ser	CAT His 145	CGC Arg	CGC Arg	CAC His	CAT His	TCT Ser 150	AAC Asn	ATA Ile	GGA Gly	TCT Ser	CTC Leu 155	GAG Glu	CGA Arg	GAC Asp	GAA Glu	660
GTG Val 160	TTC Phe	GTC Val	CCG Pro	AAA Lys	TCA Ser 165	AAG Lys	TCG Ser	AAA Lys	ATT Ile	TCA Ser 170	TGG Trp	TAT Tyr	TCT Ser	AAG Lys	TAC Tyr 175	708
TTA Leu	AAC Asn	AAC Asn	CCG Pro	CCA Pro 180	GGT Gly	CGA Arg	GTT Val	TTG Leu	ACA Thr 185	CTT Leu	GCT Ala	GCC Ala	ACG Thr	CTC Leu 190	CTC Leu	756
												GGT Gly				804
GAT Asp	CGC Arg	TTT Phe 210	GCT Ala	TGC Cys	CAT His	TAT Tyr	GAT Asp 215	CCC Pro	TAT Tyr	GGC Gly	CCA Pro	ATA Ile 220	TTT Phe	TCC Ser	GAA Glu	852
AGA Arg	GAA Glu 225	AGG Arg	CTT Leu	CAG Gln	ATT Ile	TAC Tyr 230	ATT Ile	GCT Ala	GAC Asp	CTC Leu	GGA Gly 235	ATC Ile	TTT Phe	GCC Ala	ACA Thr	900
ACG Thr 240	TTT Phe	GTG Val	CTT Leu	TAT Tyr	CAG Gln 245	GCT Ala	ACA Thr	ATG Met	GCA Ala	AAA Lys 250	GGG Gly	TTG Leu	GCT Ala	TGG Trp	GTA Val 255	948
ATG Met	CGT Arg	ATC Ile	TAT Tyr	GGG Gly 260	GTG Val	CCA Pro	TTG Leu	CTT Leu	ATT Ile 265	GTT Val	AAC Asn	TGT Cys	TTC Phe	CTT Leu 270	GTT Val	396
ATG Met	ATC Ile	ACA Thr	TAC Tyr 275	TTG Leu	CAG Gln	CAC His	ACT Thr	CAC His 280	CCA Pro	GCT Ala	ATT Ile	CCA Pro	CGC Arg 285	TAT Tyr	GGC Gly	1044
TCA Ser	TCG Ser	GAA Glu 290	TGG Trp	GAT Asp	TGG Trp	CTC Leu	CGG Arg 295	GGA Gly	GCA Ala	ATG Met	GTG Val	ACT Thr 300	GTC Val	GAT Asp	AGA Arg	1092

Asp	TAT Tyr 305	GGG Gly	GTG Val	TTG Leu	AAT Asn	AAA Lys 310	GTA Val	TTC Phe	CAT	AAC Asn	ATT Ile 315	GCA Ala	GAC Asp	ACT Thr	CAT His		1140
GTA Val 320	GCT Ala	CAT His	CAT His	CTC Leu	TTT Phe 325	GCT Ala	ACA Thr	GTG Val	CCA Pro	CAT His 330	TAC Tyr	CAT His	GCA Ala	ATG Met	GAG Glu 335		1188
GCC Ala	ACT Thr	AAA Lys	GCA Ala	ATC Ile 340	AAG Lys	CCT Pro	ATA Ile	ATG Met	GGT Gly 345	GAG Glu	TAT Tyr	TAC Tyr	CGG Arg	TAT Tyr 350	GAT Asp		1236
GGT Gly	ACC Thr	CCA Pro	TTT Phe 355	TAC Tyr	AAG Lys	GCA Ala	TTG Leu	TGG Trp 360	AGG Arg	GAG Glu	GCA Ala	AAG Lys	GAG Glu 365	TGC Cys	TTG Leu		1284
TTC Phe	GTC Val	GAG Glu 370	CCA Pro	GAT Asp	GAA Glu	GGA Gly	GCT Ala 375	CCT Pro	ACA Thr	CAA Gln	GGC Gly	GTT Val 380	TTC Phe	TGG Trp	TAC Tyr		1332
		AAG Lys		TAAA	AAAG	etg 1	CATO	TAGO	C TO	CCG							1369
	(2)	I	NFO	RMAT	ION	FOR	SE SE	Q II	ON O	:12	:						
			(i)	SEÇ (A) (B)	L	CE C ENGT YPE:	TH:		7 am	ino		lds					
				(D)		OPOI											
		(ii)	• •	T		LOGY	:	line	ar							
				MOL	ECU:	OPOI	LOGY	: :	line	ar ein	SEQ	ID 1	NO:1	.2:			
	Met 1	(xi)	MOL	ECU:	OPOI LE T	LOGY TYPE ESC	: : : p	line crot	ar ein			NO:1 Ser		Asn 15	Ser	
	1	(Gly	xi) Gly	MOL SEQ Gly	ECU: UEN: Gly 5	OPOI LE T CE D	LOGY TYPE ESC Met	: : : : : : : : : : : : : : : : : : :	rot CION	ar ein : S Val	Ile	Ile		Asn	15		
	1 Glu	(Gly	xi) Gly Lys	MOL SEQ Gly Gly 20	ECU: UENG Gly 5 Gly	OPOI LE T CE D Arg Ser	LOGY TYPE DESC Met Ser	: IRIPT	Thr Leu 25	ar ein : Val 10 Glu	Ile Arg	Ile	Ser	Asn His 30	15 Thr	Lys	
	Glu Pro	(Gly Lys Pro	Xi) Gly Lys Tyr 35	MOL SEQ Gly Gly 20	ECU: UENG Gly Gly Leu	OPOI LE T CE D Arg Ser	LOGY TYPE DESC Met Ser	: IRIPT Ser His Leu 40	Thr Leu 25 Lys	ar ein : S Val 10 Glu	Ile Arg Ala	Ile Ala Ile	Ser Pro	Asn His 30 Pro	15 Thr His	Lys Cys	
	Glu Pro	Gly Lys Pro Glu 50	xi) Gly Lys Tyr 35	MOL SEQ Gly Gly 20 Thr	ECU: UENG Gly Gly Leu Phe	OPOI LE T CE D Arg Ser Gly Val	LOGY TYPE DESC Met Ser Asn Arg	: IRIPT Ser His Leu 40 Ser	Thr Leu 25 Lys	ar ein : S Val 10 Glu Arg	Ile Arg Ala Asn	Ile Ala Ile Phe 60	Ser Pro Pro 45	Asn His 30 Pro	15 Thr His	Lys Cys Phe	
	Glu Pro Phe Cys 65	Gly Lys Pro Glu 50 Leu	xi) Gly Lys Tyr 35 Arg	MOL SEQ Gly Gly 20 Thr Ser	ECU: UENG Gly 5 Gly Leu Phe	OPOI LE T CE D Arg Ser Gly Val	Ser Asn Arg 55	: IRIPT Ser His Leu 40 Ser Ser	Thr Leu 25 Lys Phe Ile	ar ein : S Val 10 Glu Arg Ser Ala	Ile Arg Ala Asn Thr 75	Ile Ala Ile Phe 60 Asn	Ser Pro Pro 45	Asn His 30 Pro Tyr	15 Thr His Asn	Lys Cys Phe	

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu 120 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val 150 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp 200 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala 325 330 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly 345 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr

Asn Lys Ty: 385

(2)	INFOR	MATION FOR SEQ ID NO:13:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTI-SENSE: NO	
	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 123 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:13:	
TGGGTA	ATGCC	AYGANTGYGG NCA	23
(2)	INFORM	MATION FOR SEQ ID NO:14:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) TRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
ĺ	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTI-SENSE: NO	
	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 122 (D) CTHER INFORMATION: /product= "synthetic oligonucleotide"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:14:	
AAARTGI	RTGG C	CACRTGNGTR TC	22

(2)	INFORMA	TION FOR SEQ ID NO:15:
		SEQUENCE CHARACTERISTICS: (A) LENGTH: 2973 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: DNA (genomic)
	(iii)	HYPOTHETICAL: NO
	(iv)	ANTI-SENSE: NO
		ORIGINAL SOURCE: (A) ORGANISM: Arabidopsis thaliana
		IMMEDIATE SOURCE: (B) CLONE: pAGF2-6
		FEATURE: (A) NAME/KEY: exon (B) LOCATION: 433520
	, ,	FEATURE: (A) NAME/KEY: intron (B) LOCATION: 5211654
	(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:15:
ATTCGGTAAT	TCCTACATA	AT TTTAGAGATT AGTTTGAGTT TCCATCCATA CTTTACTAGT 60
GATTATAAAT	TTAAAATA	CG TACTTTCGA CTATAAAGTG AAACTAAGTA AATTAGAACG 120
TGATATTAAA	AAGTTAATO	GT TCACTGTTAT ATTTTTTCA CAAGTAAAAA ATGGGTTATT 180
TGCGGTAAAT	AAAAATACO	CA GATATTTGA ATTGATTAAA AAGGTTGAAA TAAGAGAGGA 240
GGGGAAAGAA	AAGAAGGTO	GG GGGCCCAGTA TGAAAGGGAA AGGTGTCATC AAATCATCTC 300
TCTCTCTCTC	TACCTTCGA	AC CCACGGGCCG TGTCCATTTA AAGCCCTGTC TCTTGCCATT 360
CCCCATCTGA	CCACCAGAA	AG AAGAGCCACA CACTCACAAA TTAAAAAGAG AGAGAGAGAG 420
AGAGAGACAG	AGAGAGAGA	AG AGATTCTGCG GAGGAGCTTC TTCTTCGTAG GGTGTTCATC 480
STTATTAACG	TTATCGCCC	CO TACGTOAGOT COATOTOCAG GTOOGTOGOT TOTOTTOCAT 540

TTCTTCTCAT TTTCGATTTT GATTCTTATT TCTTTCCAGT AGCTCCTGCT CTGTGAATTT

CTCCGCTCAC GATAGATCTG CTTATACTCC TTACATTCAA CCTTAGATCT GGTCTCGATT

CTCTGTTTCT CTGTTTTTT CTTTTGGTCG AGAATCTGAT GTTTGTTTAT GTTCTGTCAC

CATTAATAAT GATGAACTCT CTCATTCATA CAATGATTAG TTTCTCTCGT CTACCAAACG

600

660

720

ATATGTTGC	A TTTTCACTT	r TCTTCTTTT	TTCTAAGATO	ATTTGCTTT	G ACCAATTTGT	840
TTAGATCTT	r ATTTTATTT	ATTTTCTGGT	GGGTTGGTGG	AAATTGAAA	AAAAAAAAA	900
AAAAGCATAA	A ATTGTTATT	GTTAATGTAT	TCATTTTTTG	GCTATTTGTT	CTGGGTAAAA	960
ATCTGCTTCT	r actgttgaai	CTTTCCTGGA	TTTTTTACTC	CTATTGGGTT	TTTATAGTAA	1020
AAATACATAA	A TAAAAGGAAA	ACAAAAGTTT	TATAGATTCT	CTTAAACCCC	TTACGATAAA	1080
AGTTGGAATC	AAAATAATTO	AGGATCAGAT	GCTCTTTGAT	TGATTCAGAT	GCGATTACAG	1140
TTGCATGGAA	AATTTTCTAG	ATCCGTCGTC	ACATTTTATT	TTCTGTTTAA	ATATCTAAAT	1200
CTGATATATG	ATGTCGACAA	ATTCTGGTGG	CTTATACATC	ACTTCAACTG	TTTTCTTTTG	1260
GCTTTGTTTG	TCAACTTGGT	TTTCAATACG	ATTTGTGATT	TCGATCGCTG	AATTTTTAAT	1320
ACAAGCAAAC	TGATGTTAAC	CACAAGCAAG	AGATGTGACC	TGCCTTATTA	ACATCGTATT	1380
ACTTACTACT	AGTCGTATTC	TCAACGCAAT	CGTTTTTGTA	TTTCTCACAT	TATGCCGCTT	1440
CTCTACTCTT	TATTCCTTTT	GGTCCACGCA	TTTTCTATTT	GTGGCAATCC	CTTTCACAAC	1500
CTGATTTCCC	ACTTTGGATC	ATTTGTCTGA	AGACTCTCTT	GAATCGTTAC	CACTTGTTTC	1560
TTGTGCATGC	TCTGTTTTT	AGAATTAATG	ATAAAACTAT	TCCATAGTCT	TGAGTTTTCA	1620
GCTTGTTGAT	TCTTTTGCTT	TTGGTTTTCT	GCAGAAACAT	GGGTGCAGGT	GGAAGAATGC	1680
CGGTTCCTAC	TTCTTCCAAG	AAATCGGAAA	CCGACACCAC	AAAGCGTGTG	CCGTGCGAGA	1740
AACCGCCTTT	CTCGGTGGGA	GATCTGAAGA	AAGCAATCCC	GCCGCATTGT	TTCAAACGCT	1800
CAATCCCTCG	CTCTTTCTCC	TACCTTATCA	GTGACATCAT	TATAGCCTCA	TGCTTCTACT	1860
ACGTCGCCAC	CAATTACTTC	TCTCTCCTCC	CTCAGCCTCT	CTCTTACTTG	GCTTGGCCAC	1920
TCTATTGGGC	CTGTCAAGGC	TGTGTCCTAA	CTGGTATCTG	GGTCATAGCC	CACGAATGCG	1980
GTCACCACGC	ATTCAGCGAC	TACCAATGGC	TGGATGACAC	AGTTGGTCTT	ATCTTCCATT	2040
CCTTCCTCCT	CGTCCCTTAC	TTCTCCTGGA	AGTATAGTCA	TCGCCGTCAC	CATTCCAACA	2100
CTGGATCCCT	CGAAAGAGAT	GAAGTATTTG	TCCCAAAGCA	GAAATCAGCA	ATCAAGTGGT	2160
ACGGGAAATA	CCTCAACAAC	CCTCTTGGAC	GCATCATGAT	GTTAACCGTC	CAGTTTGTCC	2220
TCGGGTGGCC	CTTGTACTTA	GCCTTTAACG	TCTCTGGCAG	ACCGTATGAC	GGGTTCGCTT	5535
GCCATTTCTT	CCCCAACGCT	CCCATCTACA .	ATGACCGAGA	ACGCCTCCAG	ATATACCTCT	2340
CTGATGCGGG	·TATTCTAGCC	GTCTGTTTTG (GTCTTTACCG	TTACGCTGCT	GCACAAGGGA	2400
TGGCCTCGAT	GATCTGCCTC	TACGGAGTAC (CGCTTCTGAT	AGTGAATGCG	TTCCTCGTCT	2460
TGATCACTTA	CTTGCAGCAC	ACTCATCCCT (CGTTGCCTCA	CTACGATTCA	TCAGAGTGGG	2520

ACTGGCTCAG	GGGAGC'	ITTG GO	CTACCGTAG	ACAGAGACTA	CGGAATCTTG	AACAAGGTGT	2580
TCCACAACAT	TACAGAG	CACA CA	ACGTGGCTC	ATCACCTGTT	CTCGACAATG	CCGCATTATA	2640
ACGCAATGGA	AGCTACA	AAAG GO	GATAAAGC	CAATTCTGGG	AGACTATTAC	CAGTTCGATG	2700
GAACACCGTG	GTATGT	GCG AT	GTATAGGG	AGGCAAAGGA	GTGTATCTAT	GTAGAACCGG	2760
ACAGGGAAGG	TGACAA	SAAA GO	TGTGTACT	GGTACAACAA	TAAGTTATGA	GGATGATGGT	2820
GAAGAAATTG	TCGACTI	TTC TO	TTGTCTGT	TTGTCTTTTG	TTAAAGAAGC	TATGCTTCGT	2880
TTTAATAATC	TTATTGI	CCA TT	TTGTTGTG	TTATGACATT	TTGGCTGCTC	ATTATGTTAT	2940
GTGGGAAGTT	AGCGTTC	AAA TG	TTTTGGGT	CGG			2973
(2)	INFORM	ATION	FOR SEQ	ID NO:16	:		
	(i)	(A) (B) (C)	LENGTH: TYPE: STRANDE	RACTERIST: 23 base nucleic ac DNESS: si Y: linear	pairs cid ingle		
	(ii)	MOLE	CULE TYP	E: cDNA			
	(iii)	нүрот	THETICAL	: NO			
	(iv)	ANTI-	-SENSE:	NO			
	(ix)	(B)	NAME/KET	Y: misc_f N: 123 NFORMATION	: /produ "synth		
	(xi)	SEQUE	NCE DES	CRIPTION:	SEQ ID N	0:16:	
GGGCAT	GTNG A	RAANA	RRTG RTG	3			23
(2) I	NFORMA	TION	FOR SEQ	ID NO:17:			
	(i)	(A) (B) (C)	LENGTH: TYPE: r STRANDED	RACTERISTI 23 base nucleic ac DNESS: si 7: linear	pairs id ngle		
•	(ii)	MOLEC	ULE TYPE	E: cDNA			
((iii)	HYPOT	HETICAL:	: NO			

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature (B) LOCATION: 1..23

(D) OTHER INFORMATION: /product= "synthetic

oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGCATGTRC TRAANARRTG RTG

SEQUENCE LISTING

- GENERAL INFORMATION:
 - (i) APPLICANT: JONATHAN EDWARD LIGHTNER JOHN JOSEPH OKULEY
 - (ii) TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID DELTA-12 DESATURASES AND RELATED ENZYMES FROM PLANTS
 - (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTEF: MadIntosh
 (C) OPERATING SYSTEM: Microsoft Windows 95
 - (D) SOFTWARE: Microsoft Word Version 7.0
 - (vi) CURPENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: U.S. 07/977,339
 - FILING DATE: 17-NOV-1992 (B)
 - (A) APPLICATION NUMBER: U.S. 09/133,962
 - (B) FILING DATE: 14-AUG-1998
 - (viii) ATTOPNEY/AGENT INFORMATION:
 - (A) NAME: Christenbury, Lynne M..
 - (E) FEGISTRATION NUMBER: 20,971
 - (C) FEFEFENCE/DOCKET NUMBER: BB1043 US DIV
 - (ix: Telecommonication information:
 - (A) TELEPHONE: (302) 992-5481
 - TELEFAX: (301) 892-1026 (B)
 - TFLEM: 235430 (C)
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1372 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Arabidopsis thaliana
- (B) CLONE: p92103
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 93..1244
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAGAGAG ATTOTGOGGA GGAGOTTOTT OTTOGTAGGG TGTTCATCGT TATTAACGTT 60

ATCGCCCCTA CGTCAGCTCC ATCTCCAGAA AC ATG GGT GCA GGT GGA AGA ATG

Met Gly Ala Gly Gly Arg Met

 ${\tt CCG}$ GTT CCT ACT TCT TCC AAG AAA TCG GAA ACC GAC ACA AAG CGT 161

Pro Val Pro Thr Ser Ser Lys Lys Ser Glu Thr Asp Thr Thr Lys Arg 10 15 20

GTG CCG TGC GAG AAA CCG CCT TTC TCG GTG GGA GAT CTG AAG AAA GCA 209

Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys Ala 25 - 30 - 35

ATC CCG CCG CAT TGT TTC AAA CGC TCA ATC CCT CGC TCT TTC TCC TAC

ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr 40 45 50 55

CTI ATO AGI GAG AIC ATI ATA GOC TCA IGO TIO IAC TAO GIO GOC ACC - 305

Let lie ber Asprive 1.4 Le Arade. By: Fix By: $\frac{\pi}{2}$ 1 with Aspril 60 65 70

AAT TAG TTG TGT GTG GGT GAG GGT GTG TGT TAG TTG GGT TGG GCA $^{25.3}_{\pm}$

Ash Tyr Phe Ser Leu Eeu Pro Glin Pro Leu Ser Tyr Leu Ala Trp Pro 75 80 85

CTC TAT TGG GCC TGT CAA GGC TGT GTC CTA ACT GGT ATC TGG GTC ATA ± 4.4

Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile 95 100 90 GOO CAC GAA TGO GGT CAC CAC GOA TTO AGO GAC TAC CAA TGG CTG GAT 449 Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Tro Leu Asp 105 GAG AGA GTT GGT GTT ATC TTG GAT TGG TTG GTG GTG GGT TAG TTG Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe 125 130 TOO TGG AAG TAT AGT CAT CGC CGT CAC CAT TOO AAC ACT GGA TOO CTC Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu 140145 GAA AGA GAT GAA GTA TTT GTC CCA AAG CAG AAA TCA GCA ATC AAG TGG 593 Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp 155 160 TAC GGG AAA TAC CTC AAC AAC CCT CTT GGA CGC ATC ATG ATG TTA ACC ± 41 Tur Gly Lys Tyr Leu Ash Ash Pro Leu Gly Ard Ile Met Met Leu Thr 170 GTC CAG TTT GTC CTC GGG TGG CCC TTG TAC TTA GCC TTT AAC GTC TCT Val Glm Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Ash Val Ser GGC AGA COG TAT GAC GGG TTC GGT TGC CAT TTC TTC CCC AAC GGT CCC Gly Ard Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Ash Ala Pro 205 210 ATC TAC AAT GAC OGA GAA CGC CTC CAG ATA TAC CTC TCT GAT GOG GGT 7 - 5 Ile Tyr Ash Asp Arq Glu Ard Leu Gln Ile Tyr Leu Ser Asp Ala Gly 225 220 ATT CTA GCC STC TGT TTT GST CTT TAC CGT TAC GCT GCT GCA CAA GGG The Leu Ala Val Cys Phe Gly Lcu Tyr Ara Tyr Ala Ala Ala Gin Gly APG 300 TOG ATG ATC TGC OTC TAC 3GA 3TA COG CTT OTG ATA GTG AAT 991 Met Ala Ser Met Ile Cys Led Tyr Gly Val Pro Leu Leu Ile Val Asn 2 है, ह 250 260 GOG TTO OTO GTO TTG ATO ACT TAC TTG CAG CAC ACT CAT CCC TCG TTG Ala Phe Leu Val Leu Ile Thr Tyr Le. Sin His Thr His Pro Ser Leu 265 270 275

CCT CAC TAC GAT TCA TCA GAG TGG GAC TGG CTC AGG GGA GCT TTG GCT 977

Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala 280 285 290 295

ACC GTA GAC AGA GAC TAC GGA ATC TTG AAC AAG GTG TTC CAC AAC ATT 1025

Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile 300 305 310

ACA GAC ACA CAC GTG GCT CAT CAC CTG TTC TCG ACA ATG CCG CAT TAT 1073

Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr 315 320 325

AAC GCA ATG GAA GCT ACA AAG GCG ATA AAG CCA ATT CTG GGA GAC TAT 1121

Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp Tyr 330 335 340

TAC CAG TTC GAT GGA ACA CCG TGG TAT GTA GCG ATG TAT AGG GAG GCA 1169

Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala 345 - 350 - 355

AAG GAG TGT ATC TAT GTA GAA CUG GAU AGG GAA GGT GAC AAG AAA GGT 1217

Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys Gly 360 370 375

GTG TAC TGG TAC AAC AAT AAG TTA TGAGCATGAT GGTGAAGAAA TTGTCGACCT

Val Tyr Trp Tyr Asn Asn Lys Leu 380

TTCTCTTGTC TGTTTGTCTT TTGTTAAAGA AGCTATGCTT CGTTTTAATA ATCTTATTGT 1331

CCATTTGTT GTGTTATGAC ATTTTGGCTG CTCATTATGT T 1372

(1) INFORMATION FOR SEQ 10 NO:2:

- (i) SEQUENCE CHAPACTERISTICS:
- (A neivoln: bet aming ablån
- (B) TYPE: amino acid
- (U) ISPUNUGI: Ilneal
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser

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Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gin Gly Cys Val Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 135 His Ser Ash Thr Gly Ser Let Glu Ard Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Ash Ash Pro Leu 165 Gly Ard Ile Met Met Leu Thr Val Glr. Fhe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln 215 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Ard Tyr Ala Ala Ala Clo Cly Met Ala Ser Met Ile Cvs Leu Tyr Glw Val Pro Let ben 71e Var Ash Ala Pho Leo var Lou 11e Int lyr Leo 275 Gla His Thr His Pro Ser Lee. Pro His Tyr Asp Ser Ser Glu Tro Asp 280 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Ash Lys Val Phe His Ash The Thr Asp Thr His Vat Ala His His Lou

305		310		315		320
Phe Ser	Thr Met Pro	His Tyr Asn	Ala Met 330	Glu Ala T	hr Lys Ala 335	
Lys Pro	Ile Leu Gly 340	Asp Tyr Tyr	Gln Phe 345	Asp Gly T	hr Pro Trp 350	Tyr
Val Ala	Met Tyr Arg 355	Glu Ala Lys 360	Glu Cys		al Glu Pro 65	Asp
Arg Glu 370	Gly Asp Lys	Lys Gly Val	Tyr Trp	Tyr Asn A	sn Lys Leu	
(2)	INFORMATION	FOR SEQ ID 1	:6:00			
	(A) LENGTH: (B) TYPE: ra	DNESS: single	airs	S:		
	(ii) MOLI	ECULE TYPE:	oDNA to	mP.NA		
	(iii) HYP	OTHETICAL: 1	4 0			
		GINAL SOURCE: M: Brassica :				
	(A) NAME/KE	FURE: f: CDS n: 1301284				
	(xi) SEQ	JENCE DESCRI	PTION: S	SEQ ID NO:	3 :	
GGCACGAC	GCT CGTGCCGA	AT TOGGCACGAC	G AGGAGAC	CAGA GAGAG	AGTTT GAGG	AGGAGC 60
TTCTTCG	TAG GGTTCATO	GT TATTAACGT	r AAATGTI	TCAT CCCCC	CCTAC GTCA	GCCAGC 120
TCAAGAAA		CA GGT GGA AG la Gly Gly Ar S			Pro Pro 3	
		GAC AAC ATC Asp Asn lle				
		GAA CIC AAG Glu Leu Lys 35				
		aga mam mma Ang Ser Phe				Ile
n m n	ma casta i massasta i mampila		A Section of the con-	and the second of the second of	mana sajama sajaja	

Ile	Ala	Ser	Cys 65	Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	
				TCC Ser												408
				ACC Thr												456
				GAC Asp												504
				CTC Leu 130												552
				TCC Ser												600
				AAG Lys												648
				OGC Arg											GGC Gly	୧୨ଟ
				TTA Leu												744
				CAT His 210												792
GAG Glu	OGT Arg	cTc Leu	CAG Gln 225	ATA Ile	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	GCT Ala	GGC Gly	ATC Ile	CTC Leu	GDO Ala 235	GTC Val	TGC Cys	840
				CGC Ary												88h
				GTT Fai												236
				CAG Gln												98.1
TUT	GAŞ	TGG	GAT	TĞG	TTG	AGG	GGA	-; <u>::</u>	TTG	(3/2/2	A/····	amm	(AC)	AGA	GAC	1937

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Ser Glu Trp Asp Trp Leu Arg Gly A	
290	295 300
TAC GGA ATC TTG AAC AAG GTC TTC CA Tyr Gly Ile Leu Asn Lys Val Phe H: 305	
GCG CAT CAC CTG TTC TCG ACC ATG Co Ala His His Leu Phe Ser Thr Met P: 320 325	
ACG AAG GCG ATA AAG CCG ATA CTG GC Thr Lys Ala Ile Lys Pro Ile Leu G 335 · 340	
ACG CCG GTG GTT AAG GCG ATG TGG A	GG GAG GCG AAG GAG TGT ATC TAT 12
24 Thr Pro Val Val Lys Ala Met Trp A: 350 355	ng Glu Ala Lys Glu Cys Ile Tyr 360 365
GTG GAA CCG GAC AGG CAA GGT GAG AA	AG AAA GGT GTG TTC TGG TAC AAC 12
73 Val Glu Pro Asp Arg Gln Gly Glu L 370	vs Lys Gly Val Phe Trp Tyr Asn 375 380
AAT AAG TTA TGA AGCAAAGAAG AAACTGA	AGC TTTCTCTTCT ATGATIGTCT 13
- 24 - Ash bys beu	
TTGTTTAAGA AGCTATGTTT CTGTTTCAAT : 84	ATCTTAATT ATCCATTTTG TTGTGTTTTC 13
TGACATTTTG GCTAAAATTA TGTGATGTTG : 26	SAAGTTAGTG TC 14
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTER (A) LENGTH: 384 amine acid (B) TYPE: amine acid (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: pr	etein
(xi) SEQUET E DESTRIFT	=0N: .:EQ I(0 No:4:
Met Gly Ala Gly Gly Arg Met Gln V	al Ser Pro Pro Ser Lys Lys Ser
Glu inr Asp Ash lle Lys Arg Val P	to Cys Glu Thr Pro Pro Phe Thr
Val Gly Glu Leu Lys Lys Ala Ile P. 35	oo Pro His Cys Phe Lys Arg Ser 45

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Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Ard Thr Val Met Leu Thr Val Glr. Phe Thr Leu Gly Trp Pro Leu 180 150 Tyr Leu Ala Phe Ash Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys His Phe His Pro Asr. Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 Gly Val Pro Leu Leu Ile Val Asr. Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Let Ard Gly Ala Leu Ara Thr Val Asp Ard Asp Tyr Gly Ile Lou Ash Lys .u. the Hit wan i.e .hr Asy inf His Val Ala His His 315 305 310 Len Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Tys Ala 330 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 34% Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 375 380

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Glycine max
 - (vii) IMMEDIATE SOUPCE:
 - (B) CLONE: psF2-165F
 - (ix) FEATURE:
 - (A) NAME/HEY: CDS
 - (B) LOCATION: 105..1247
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATATACTA ATATTTGCTT GTATTGATAG CCCCTCCGTT CCCAAGAGTA TAAAACTGCA

TOGAATAATA CAAGOCAGTA GGCATGGGTC TAGCAAAGGA AACAACA ATG GGA GGT 116

Met Gly Gly

AGA GGT CGT GTG GCC AAA GTG GAA GTT CAA GGG AAG AAG CCT CTC TCA

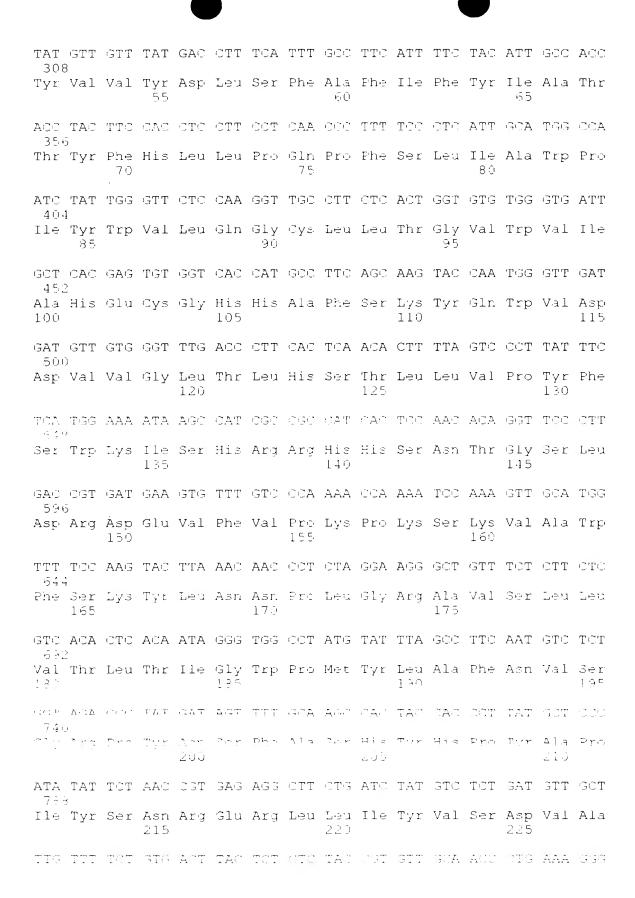
Ard Gly Ard Val Ala 50s Val Glu Val Glu Glv 5ys 5vs Pro Leu Ser

AGG GIL JUA AAN AWA AWA JÜA LUA İTU AWT YTT BAY WAA JIC AAG AAA Dang

Arg Val Pro Asi. Thi Lys Fro Fro Fle Thi Val Gly Gli Leu Lys Lys 20 35

GEN ATT CEN CON CASE THE TITE DAG OFF THE CITE OFF ACT THAT THE THE $2\,60$

Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser 40 45 50



936 Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys Gly 230 235 240 TTG GTT TGG CTG CTA TGT GTT TAT GGG GTG CCT TTG CTC ATT GTG AAC Leu Val Trp Leu Leu Cys Val Tyr Gly Val Fro Leu Leu Ile Val Asn 245 GGT TTT CTT GTG ACT ATC ACA TAT TTG CAG CAC ACA CAC TTT GCC TTG Gly Phe Leu Val Thr Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu 265 270 CCT CAT TAC GAT TCA TCA GAA TGG GAC TGG CTG AAG GGA GCI TTG GCA 980 Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala 230 285 ACT ATG GAC AGA GAT TAT GGG ATT CTG AAC AAG GTG TTT CAT CAC ATA 1028 Thr Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile 295 300 305 ACT GAT ACT CAT GTG GCT CAC CAT CTC TTC TCT ACA ATG CCA CAT TAC 13.00 The Ase Thr His Val Ala His His Let Phe Ber Thr Met Pro His Tyr 310 315 CAT GCA ATG GAG GCA ACC AAT GCA ATC AAG CCA ATA TTG GGT GAG TAC His Ala Met Glu Ala Thr Ash Ala Ile Lys Pro Ile Leu Gly Glu Tyr TAC CAA TIT GAT GAC ACA CCA TIT TAC AAG GCA CIG IGG AGA GAA GCG 1173 Tyr Gln Phe Asp Asp Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala 350 355 345 AGA GAG TGC CTC TAT GTG GAG CCA GAT GAA GGA ACA TCC GAG AAG GGC 1210 Arm Glu Cys Leu Tyr Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly 360 GTG TAT TGG TAC AGG AAC AAG TAT TGATGGAGCA ACCAATGGGC CATAGTGGGA 157.1 Val Tyr Trp Tyr Aig Ash Lys Tyl

OTTATGGAAG TITTGTCATG TATTAGTACA TAATTAGTAG AATGTTATAA ATAAGTGGAT

TTGCCGCGTA ATGACTTTGT GTGTATTGTG AAACAGCTTG TTGCGATCAT GGTTATAATG

TARARATARI TUTGGTATTA ATTACATUTG GAMAGISTIL IL TITTATALL TITCIGOCTA

1454

AAAAAAA 1462

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (11) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Arg Gly Arg Val Ala Lys Val Glu Val Gln Gly Lys Lys 1 5 10 15

Pro Leu Ser Arg Val Pro Asn Thr Lys Pro Pro Phe Thr Val Gly Gln 20 25 30

Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Thr 35 40 45

Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala Phe Ile Phe Tyr 50 55

Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Glr. Pro Phe Ser Leu Ile65707580

Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu Leu Thr Gly Val

Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Lys Tyr Gln

Trp Val Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val

Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr 130 135 140

Gly Ser Leu Asp Ard Asp Glu Val Phe Val Pro Lys Pro Lys Ser Lys 145 - 155 - 166

For Ald Ity Thy set syn lyn 212 Air Afric. 171 174 try Afg Ald (4. 175

Ser Leu Leu Val Thr Leu Thr Ile Gly Tro Pro Met Tyr Leu Ala Phe 180 185 190

Asn Val Ser Gly Arg Pro Tyr Asp Ser Phe Ala Ser His Tyr His Pro 195 200 205

Tyr Aid Fro Ile Tyr Ser Ash Arg Hu Arg Leu Leu Ile Tyr Val Ser

210 215 220

Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val Ala Thr 225 230 235 240

Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Gln His Thr His 260 265 270

Phe Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly 275 286 285

Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe 290 295 300

His His Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met 305 310 315 320

Pro His Tyr His Ala Met Glu Ala Thr Asn Ala Ile Lys Pro Ile Leu 325 330 335

Gly Glu Tyr Tyr Gln Phe Asp Asp Thr Pro Phe Tyr Lys Ala Leu Trp 340 345 350

Arg Glu Ala Arg Glu Cy* L-u Tyr Vei Glu Pro Asp Glu Gly Thr Ser 355 360 360

Glu Lys Gly Val Tyr Trp Tyr Arg Asn Lys Tyr 370

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1730 base pairs
- (B) TYPE: nucle:c acid
- (C) STRANGEDMESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (LV) ANTI-CENSE: No

(A) OFGANISM: Zea mays

(vii) IMMEDIATE SOURCE:

(B) CLONE: pFad.#1

(ix) FEATURE:

(A) NAME/HEY: CDS

(B) LOCATION: 165..1328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGCCTCTCC CCTCCCTCCT CCCTGCAAAT CCTGCAGACA CCACCGCTCG TTTTTCTCTC 60

CSGGACAGGA GAAAAGGGGA GAGAGAGGTG AGGCGCGGTG TCCGCCCGAT CTGCTCTGCC 120

degacgeage tettaceace tectcaetet caetcaegae caas ate eet ecc ege $17.6\,$

Met Gly Ala Gly

Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg 5 10 15 15 20

GOT ACC GGT GGC GCC GCG ATG CAS CGG TCG CCG GTG GAG AAG CCT CCG - 272

Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val Glu Lys Pro Pro 25 30 35

TTC ACT CTG GGT CAG ATC AAG AAG GCC ATC CCG CCA CAC TGC TTC GAG $^{\circ}$ 310

Phe Thr Gen Gly Gln Ile Lys Bys Ala Ile Pro Pro His Cys Phe Glu 47 45 50

CGC TCG GTG CTC AAG TCC TTC TCG TAC GTG GTC CAC GAC CTG GTG ATC 383

Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His Asp Leu Val Ile 55 60 65

See GCG GCG CTC CTC TAC TTC GCG CTG GCC ATC ATA CCG GCG CTC CCA 416 .

Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile Pro Ala Leu Pro 70 75 30

AGG CCG CTC CGC TAC GCC GCC TGG CCG CTG TAC TGG ATC GCG CAG GGG 474

Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly -85 90 95 100

THE STREET AND REST RESTRICT ATO GOT CAR RAGINGS GGC CAR CAR STREET FOR STREET RESTRICT REST

of Val C, s The Gry Val Too Val IIV Ala His blu Cyc Cly His His

GOUNTION THE GAO TAC TOP CTC CTP GAO GAO STG GTC GGO CTP GTG CTP

Ala Phe Ser Asp Tyr Ser Led Leu Asp Asp Val Val Gly Leu Val Leu 120 125 130

CAG TOG TOG OTO ATG GTG COO TAC TTO TOG TGG AAG TAC AGO CAD OGG

His Ger Ser Len Met Val Fro Tyr Pho Ser Trp Lys Tyr Ser His Arg

	135					140					145			
CGC CAC	CAC	TCC	AAC	ACG	GGG	TCC	CTG	GAG	CGC	GAC	GAG	GTG	TTC	GTG
Arg His	His	Ser	Asn	Thr	Gly 155	Ser	Leu	Glu	Arg	Asp 160	Glu	Val	Phe	Val
CCC AAG	AAG	AAG	GAG	GCG	CTG	CCG	TGG	TAC	ACC	CCG	TAC	GTG	TAC	AAC
Pro Lys 165	Lys	Lys	Glu	Ala 170	Leu	Fro	Trp	Tyr	Thr 175	Pro	Tyr	Val	Tyr	Asn 180
AAC CCG 752	GTC	GGC	CGG	GTG	GTG	CAC	ATC	GTG	GTG	CAG	CTC	ACC	CTC	GGG
Asn Pro	Val	Gly	Arg 185	Val	Val	His	Ile	Val 190	Val	Gln	Leu	Thr	Leu 195	Gly
TGG CCG 800	ÇTG	TAC	CTG	GCG	ACC	AAC	GCG	TCG	GGG	CGG	CCG	TAC	CCG	CGC
Trp Pro	Leu	Tyr 200	Leu	Ala	Thr	Asn	Ala 205	Ser	Gly	Arg	Pro	Tyr 210	Pro	Arg
TTC GCC	TGC	CAC	TTC	GAC	CCC	TAC	GGC	CCC	ATC	TAC	AAC	GAC	CGG	GAG
Phe Ala	Cys 215	His	Fhe	Asp	Pro	Tyr 220	Gly	Pro	Ile	Туг	Asn 225	Asp	Arg	Glu
060 600 896	CAG	ATC	TTC	GTC	TCG	GAC	GCC	GGC	GTC	GTG	GCC	GTG	GCG	TTC
Arg Ala 230	Gln	Ile	Fhe	Val	Ser 235	Asp	Ala	Gly	Val	Val 240	Ala	Val	Ala	Phe
GGG CTG 944	TAC	AAG	CTG	GCG	GCG	GCG	TTC	GGG	GTC	TGG	TGG	GTG	GTG	CGC
Gly Leu 245	Tyr	Lys	Leu	Ala 250	Ala	Ala	Phe	Gly	Val 255	Trp	Trp	Val	Val	Arg 260
GTG TAC 992	GCC	GTG	CCG	CTG	CTG	ATC	GTG	AAC	GCG	TGG	CTG	GTG	CTC	ATC
Val Tyr	Ala ·		Pro 265		Leu	Ile		Asn 270		Trp	Leu	Val	Leu 275	
ACC TAC 1040	CTG	CAG	CAC	ACC	CAC	CCG	TOG	CTC	CCC	CAC	TAC	GAC	TCG	AGC
Inr Tyr	Leu	Gin 280	His	Tnr	ніз	Fro	Ser 233	Leu	Pro	Hıs	Гуr	Asp 291	ser	Ser
GAG TGG 1983	GAC	TGG	· . T.: 4	17(717)	GGC	() r	CTE	G() 1	ACC	ATS	GAC	CGC	GAC	ГАС
Glu Trp	Asp 295	Trp	Leu	Arg	Gly	A1a 300	Leu	Ala	Thr	Met	305	Arg	Asp	Tyr
GGC ATC	CTC	AAC	CGC	GTG	TTC	CAC	AAC	ATC	ACG	GAC	ACG	CAC	GTC	GCG
Gly Ile 310	Leu	Asn	Arg	Val	Phe 315	His	Asr.	Ile	Thr	Asp 320	Thr	His	Val	Ala



His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr 325 330 335 340

AAG GOG ATO AGG COO ATO CTO GGO GAO TAO FAO CAO TTO GAO COG ACO

Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Pro Thr 345 350 355

CCT GTC GCC AAG GCG ACC TGG CGC GAG GCC GGG GAA TGC ATC TAC GTC 1280

Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu Cys Ile Tyr Val 360 365 370

GAG COC GAG GAC CGC AAG GGC GTC TTC TGG TAC AAG AAG AAG TTC TAGCCGCCG C 1335

Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn Lys Lys Phe 375 380 385

CGCTCGCAGA GCTGAGGACG CTACCGTAGG AATGGGAGCA GAAACCAGGA GGAGGAGACG 1395

STACTOSCOC CAAAGTOTOO GTCAACOTAT CTAATOGTTA GTCGTCAGTC TTTTAGACGG 1455

GAAGAGAGAT CATTTGGGCA CAGAGACGAA GGCTTACTGC AGTGCCATCG CTAGAGCTGC 1815

CATCAAGTAC AAGTAGGCAA ATTCGTCAAC TTAGTGTGTC CCATGTTGTT TTTCTTAGTC

GTCCGCTGCT GTAGGCTTTC CGGCGGCGGT CGTTTGTGTG GTTGGCATCC GTGGCCATGC 1638

CTGTGCGTGC GTGGCCGCGC TTGTCGTGTG CGTCTGTCGT CGCGTTGGCG TCGTCTCTTC

GTGCTCCCCG TGTGTTGTTG TAAAACAAGA AGATGTTTTC TGGTGTCTTT GGCGGAATAA 1755

CAGATOGTOC GAACGAAAAA AAAAAAAAAA AAAAA 1790

- (2) INFORMATION FOR SEQ ID NO:3:
 - (1) SPONENCE CHARACTERISTICS:
 - (A) LENGTH: :8% amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Glu Arg Ser Val Lou Lys Ser Phe Ser Tyr Val Val His Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly Cys Val Cys Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val 115Gly Leu Val Leu His Ser Ber Lou Met Val Pro Tyr Phe Ser Trp Lys 1.35 Tyr Ser His Arg Arg His His Ser Ash Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro Tyr Val Tyr Asr. Asn Pro Val Gly Arg Val Val His Ile Val Val Gln 185 Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Ash Ala Ser Gly Arg 195 200 Pro Tyr Pro Ang Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr Ash Asp Arg Glu Arg Ala Gln II. Phe Val Ser Asp Ala Gly Val Val A a Val Ala Phe Glv Leu Tvr Dw. Leu Ala Ala Ala Pho Gly Val Trp Tip Val Val Arg Wal Tyr Alâ Vo. Fib Leu Lêu Ile Val Ast. Ala Tip 260 Lau Val Lau Ile Thr Tyr Lou Si: His Thr His Pro Ser Lou Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met

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Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp 305 310 315 320

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala 325 330 335

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His 340 345 350

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu 355 360 365

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn 370 380

Lys Lys Phe 335

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: dDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) OFGANISM: Ficinus communis
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pRF2-1C
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..673

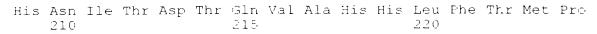
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TTG CTT GAT GAT GTA GTT GGT CTT ATC CTA CAC TCC TGT CTC CTT GTC

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val 20 25 30

TOT TAT TIT TOA TOG AMA CAO AGO TAT TIGO TOA TAT TOO AAC ACA

144 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr 35 40 GGG TCC CTG GAA CGG GAT GAA GTG TTT GTT CCC AAG AAG AAA TCT AGT 1.92 Gly Ser Leu Glu Ard Asp Glu Val Phe Val Pro Lys Lys Ser Ser ATC CGT TGG TAT TCC AAA TAC CTC AAC AAC CCT CCA GGT CGT ATC ATG Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met 7.5. 7.0 ACA ATT GCC GTC ACA CTT TCA CTT GGC TGG CCT CTG TAC CTA GCA TTC 288 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe 90 AAT GTT TOA GGC AGG COA TAT GAT CGG TTC GCC TGC CAC TAT GAC CCA 336 Asr. Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro 100 105 110 THI GGC COG ATC THE HAT GAT CGC GAG OGA ATC GAG ATA TIC ATA TOA Thr Gly Profile Tyr Ash Asb Ard Glu Ard ile Glu Mie Dae Ile Ser 115 120 GAT GCT GGT GTT CTT GCT GTC ACT TTT GGT CTC TAC CAA CTT GCT ATA Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile 1.3:0 GOG AAG GGG CTT GCT TGG GTT GTC TGT GTA TAT GGA GTG CCA TTG TTG Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu 155 150 160GTG GTG AAT TOA TTO CTT GTT CTG ACO TTT CTG CAG CAT ACT CAC 528 Val Val Asm Ser Phe Leu Val Leu The Thr Phe Leu Gln His Thr His 165 CCT GCA TTG CCA CAT TAT GAT TCG TCG GAG TGG GAC IGG CIA AGA GGA 17.5 aro Ala Leu Bro His Tyr Asp der des dia Ingolago Digoles Guy aly 130 135 GOT OTA GOA ACT GTT GAC AGA GAT TAC GGG ATC TTG AAC AAG GTG TTG Ala Leu Ala Thr Val App Arg Asp Fyr Gly Ile Lou Ash Lys Val Phe 195 205 CAT AAC ATA AGG GAG ACT CAA GTA GOT CAC CAG CTT TTC AGC ATG COC C



- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
1 10 15

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val 20 25 30

Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr 35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Ser Ser 50 55

lle Arg Trp Tyr Ser Lys Tyr heu Asr Ash Pro Pro Gly Arg Ile Mot -65 /0 /5 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe 85 90 95

Ash Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro

Tyr Gly Pro Ile Tyr Asr. Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile 130 135 140

Ala Lys Gly Leu Ala T:p Val Val Cys Val Tyr Gly Val Pro Leu Leu 145 - 156 - 155

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Tro Asp Trp Leu Ard Gly 180 - 180

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe 195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro 210 215 220

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) OFGANISM: Ricinus communis
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pRF197c-42
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 184..1347
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- CGGCCGGGAT TCCGGTTTTC ACACTAATTT CCAAAAAATG CATGATTTCA CCTCAAATCA
- AACACCACAC CTTATAACTT AGTCTTAAGA GAGAGAGAGA GAGGAGACAT TTCTCTCTC
- TGAGATGAGC ACTICICITC CAGACATCGA AGCCTCAGGA AAGTGCTTGA GAAGAGCTTG
- AGA ATG GGA GGT GGT GGC ATG TOT ACT GTC ATA ATC AGC AAC AAC
 - Met Gly Gly Gly Ard Met Ser Thr Val Ile Ile Ser Asn Asn 1 5 10 15
- AGT GAG AAG AAA BGA BGA AGC AGC CAC CTG GAG CGA GCG CCG CAC ACG - 178
- Ser Glu Lys Lys Gly Gly Ser Ser His Leu Glu Arg Ala Pro His Thr 20 25 30
- AAG COT COT TAY ADA OFF BEF ARD DIG AAB ABA GOU ATO COA DOD CAF
- Lvs Pro Pro Tvr Tnr Leu Gly Ash Leu Lys Ard Ala Ile Pro Pro His
- TGC TTT GAA CGC TCT TTT GTG CGC TCA TTC TCC AAT TTT GCC TAT AAT $^{3.72}$
- Cys Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Asn Phe Ala Tyr Asn 50 55 60
- TTO TGO TTA AGT TTT CTT TOO TAC TOO ATO GOO AND AAC TTO TTO CCT

420 Phe Cys Leu Ser Phe Leu Ser Tyr Ser Ile Ala Thr Asn Phe Phe Pro 7.0 TAC ATC TCT TCT CCG CTC TCG TAT GTC GCT TGG CTG GTT TAC TGG CTC Tyr Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu 85 90 TTC CAA GGC TGC ATT CTC ACT GGT CTT TGG GTC ATC GGC CAT GAA TGT Phe Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys 100 105 GGC CAT CAT GCT TTT AGT GAG TAT CAG CTG GCT GAT GAC ATT GTT GGC 564 Gly His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly 115 120 CTA ATT GTC CAT TCT GCA CTT CTG GTT CCA TAT TTT TCA TGG AAA TAT 612 Leu Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr 130 135 AGC CAT CGC CGC CAC CAT TCT AAC ATA GGA TCT CTC GAG CGA GAC GAA 660 Ser His Arg Ard His His Ber Ash Ile Gly Ber Leu Glu Arg Asp Glu 150 GTG TTC GTC CCG AAA TCA AAG TCG AAA ATT TCA TGG TAT TCT AAG TAC Val Phe Val Fro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr 175 TTA AAC AAC CCG CCA GGT CGA GTT TTG ACA CTT GCT GCC ACG CTC CTC Leu Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu 180 135 190 CTT GGC TGG CCT TTA TAT TTA GCT TTC AAT GTC TCT GGT AGA CCT TAC 904Leu Gly Trp Fro Leu Tyr Leu Ala Phe Ash Val Ser Gly Arg Pro Tyr 195 200 GAT CGC TTF GCT TGC CAT TAT GAT CCC TAT GGC CCA ATA TTT TCC GAA = 52 Aup ing the Alestyo institut Aup red lyr Aly is tale the destalu 210 AGA GAA AGG CTT CAG ATT TAC ATT GCT GAC CTC GGA ATC TTT GCC ACA Arg Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr 230 235 225 ACG TTT GTG CTT TAT CAG GCT ACA ATG GCA AAA GGG TTG GCT TGG GTA

Thr Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val 245 250 255 ATG CGT ATC TAT GGG GTG CCA TTG CTT ATT GTT AAC TGT TTC CTT GTT Met Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val 265 260 ATG ATC ACA TAC TTG CAG CAC ACT CAC CCA GCT ATT CCA CGC TAT GGC 1044 Met Ile Thr Tyr Leu Gln His Thr His Fro Ala Ile Pro Arg Tyr Gly 280 275 TCA TCG GAA TGG GAT TGG CTC CGG GGA GCA ATG GTG ACT GTC GAT AGA 1092 Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg 290 295 GAT TAT GGG GTG TTG AAT AAA GTA TTC CAT AAC ATT GCA GAC ACT CAT 1140 Asp Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His 310 305 GTA GCT CAT CAT CTC TTT GCT ACA GTG CCA CAT TAC CAT GCA ATG GAG 1138 Val Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu 330 335 GOO ACT AAA GOA ATO AAG OOT ATA ATG GGT GAG TAT TAC OGG TAT GAT Ala Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp 340 GGT ACC CCA TTT TAC AAG GCA TTG TGG AGG GAG GCA AAG GAG TGC TTG 1284 Gly Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu 355 360 ITC GTC GAG CCA GAT GAA GGA GCT CCT ACA CAA GGC GTT TTC TGG TAC 1332 Phe Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr 375 370 CGG AAC AAG TAT TAAAAAAGTG TOATGTAGCO TGCCG エろもタ Arg Asn Lys Ty:

- 2. INFORMATION FOR JEQ ID No:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii Maleoule Type: pr 'ein

BB1043 US CNT1 Seq listing.txt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Gly Gly Gly Arg Met Ser Thr Val Ile Ile Ser Asn Asn Ser 1.0 Glu Lys Lys Gly Gly Ser Ser His Leu Glu Arg Ala Pro His Thr Lys Pro Pro Tyr Thr Leu Gly Asn Leu Lys Arg Ala Ile Pro Pro His Cys Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Ash Phe Ala Tyr Ash Phe Cys Leu Ser Phe Leu Ser Tyr Ser Ile Ala Thr Ash Phe Phe Pro Tyr Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly 100 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu 170 Ash Ash Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu Tyr Leu Ala Phe Ash Val Ser Gly Arg Prc Tyr Asp 200 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg The Tour Time Turn the Ala The Thr 230 200 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Hie Tyr Jly Val Pro Leu Leu Ile Val As.. Cyl Tho Lou Val Met The Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp 295 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val 315 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala 325 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly 340 345 350 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe 3.60 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr 385 INFORMATION FOR SEQ ID NO:13: (2)(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs TYPE: nualeic arid STRAMDEDMESS: single (C)(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO FEATURE: (ix) (A) NAME/REY: misc_feature(B) LOCATION: 1..23(D) OTHER INFORMATION: /product= "synthetic oligonucleotide" *xi' ENPUENTE OFSCRIPTION: SEO ID NO:13:

23

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(1) SEQUINCE CHAPACTERISTICS:

- (A) LENGTH: 22 base pairs
- (D) TYPE: musleis acld
- (C) TRANDEDNESS: single
- (D) TOPOLOGY: linear
- 111) MCLECULE TYPE: MINA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO
<pre>(ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 122 (D) OTHER INFORMATION: /product= "synthetic oligonuclectide"</pre>
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
AAARTGRTGG CACFTGNGTR TC 22
(2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 2973 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
(ii) MODECULE TYPE: DNA (genomic)
(111) militarization mo
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE: (A) ORGANISM: Arabidopsis thaliana
(vii) IMMEDIATE SOURCE: (E) CLONE: pAGF2-6
(ix) FEATURE: (A) NAME/FEY: exch (B) LOCATION: 433520
(ix) FEATURE: (A) NAME/MEY: intron (B) LOCATION: 5211854
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
ATTOGGTAAT TO STACATAT FTTAGAGAIT AGTTTGAGIT IJONIQUATA JITTAJIAJ
GATTATAAAT ITAMAATADG TAGUTTTOBA OTATAAAGTG AAAGTAAGTA AATTAGAACG 1
TGATATTAAA AAGTTAATGT TOACTGTTAT ATTTTTTTOA CAAGTAAAAA ATGGGTTATT 80
TGCGGTAAAT AAAAATACCA JATATTTTGA ATTGATTAAA AAGGTTGAAA TAAGAGAGGA

40

GGGGAAAGAA 90	AAGAAGGTGG	GGGCCCAGTA	TGAAAGGGAA	AGGTGTCATC	AAATCATCTC	3
TOTOTOTOTO 50	TACCTTCGAC	CCACGGGCCG	TGTCCATTTA	AAGCCCTGTC	TCTTGCCATT	3
CCCCATCTGA 20	CCACCAGAAG	AAGAGCCACA	CACTCACAAA	TTAAAAAGAG	AGAGAGAGAG	4
AGAGAGACAG 80	AGAGAGAGAG	AGATTOTGOG	GAGGAGCTTC	TTCTTCGTAG	GGTGTTCATC	-1
GTTATTAACG 40	TTATCGCCCC	TACGTCAGCT	CCATCTCCAG	GTCCGTCGCT	TCTCTTCCAT	5
TTCTTCTCAT 00	TTTCGATTTT	GATTCTTATT	TCTTTCCAGT	AGCTCCTGCT	CTGTGAATTT	ťō
CTCCGCTCAC 60	GATAGATCTG	CTTATACTCC	TTACATTCAA	CCTTAGATCT	GGTCTCGATT	ő
OTOTGTTTOT	CTGTTTTTT	CTTTTGGTCG	AGAATCTGAT	GTTTGTTTAT	GTTCTGTCAC	7
80 - Danavarvar.	<i>بخانا شدی</i> ۷ میست. بازد	CICATICATA	CAATGATTAG	TTTCTCTCGT	CTACCAAACG	,
ATATGTTGCA	TTTTCACTTT	TOTTOTTTTT	TTCTAAGATG	ATTTGCTTTG	ACCAATTTGT	8
TTAGATCTTT	ATTTATTTT	ATTTTCTGGT	GGGTTGGTGG	AAATTGAAAA	AAAAAAAA	Ģ
AAAAGCATAA EO	ATTGTTATTT	GTTAATGTAT	TCATTTTTTG	GCTATTTGTT	CTGGGTAAAA	9
ATCTGCTTCT	ACTGTTGAAT	CTTTCCTGGA	TTTTTTACTC	CTATTGGGTT	TTTATAGTAA	10
AAATACATAA RO	TAAAAGGAAA	ACAAAAGTTT	TATAGATTCT	CTTAAACCCC	TTACGATAAA	10
AGTTGGAATC i	AAAATAATTO	AGGATCAGAT	GCTCTTTGAT	TGATTCAGAT	GCGATTACAG	ŢŢ
OO mmaaamaaakk	७% के के के के के के किया के किया के किया के किया के किया किया किया किया किया किया किया किया	$\sum_{i=1}^n \hat{W}_i \hat{W}$	Δαλάμττντ	ттстстттка	ATATUTAAAT	1.2
OTGATATATG	ATGTCGACAA	ATTCTGGTGG	CTTATACATC	ACTTCAACTG	TTTTCTTTTG	12
GCTTTGTTT:G 20	TCAACTTGGT	TTTCAATACG	ATTTGTGATT	TOGATOGOTS	AATTTTTAAT	13

ACAAGCAAAC 80	TGATGTTAAC	CACAAGCAAG	AGATGTGACC	TGCCTTATTA	ACATOGTATT	13
ACTTACTACT 40	AGTOGTATTO	TCAACGCAAT	CGTTTTTGTA	TTTCTCACAT	TATGCCGCTT	14
CTCTACTCTT 00	TATTCCTTTT	GGTCCACGCA	TTTTCTATTT	GTGGCAATCC	CTTTCACAAC	15
CTGATTTCCC 60	ACTTTGGATC	ATTTGTCTGA	AGACTCTCTT	GAATCGTTAC	CACTTGTTTC	15
TTGTGCATGC 20	TCTGTTTTTT	AGAATTAATG	ATAAAACTAT	TOCATAGTOT	TGAGTTTTCA	16
GCTTGTTGAT 80	TOTTTTGOTT	TTGGTTTTCT	GCAGAAACAT	GGGTGCAGGT	GGAAGAATGC	16
CGGTTCCTAC 40	TTCTTCCAAG	AAATCGGAAA	CCGACACCAC	AAAGCGTGTG	CCGTGCGAGA	17
AACCGCCTTT 00	CTCGGTGGGA	GATCTGAAGA	AAGCAATCCC	GOOGCATTGT	TTCAAACGCT	18
CAATCCCTCG CC	CTCTTTCTCC	TATTCOAT	GTGACATCAT	TATAGCCTCA	TGCTTCTACT	18
ACGTCGCCAC 30	CAATTACTTC	TOTOTOOTOO	CTCAGCCTCT	CTCTTACTTG	GCTTGGCCAC	13
TOTATTGGGC 80	CTGTCAAGGC	TGTGTCCTAA	CTGGTATCTG	GGTCATAGCC	CACGAATGCG	19
GTCACCACGC 40	ATTCAGCGAC	TACCAATGGC	TGGATGACAC	AGTTGGTCTT	ATCTTCCATT	20
COTTOCTCCT 66	CGTCCCTTAC	TTCTCCTGGA	AGTATAGTCA	TOGCCGTCAC	CATTCCAACA	21
OTGGATCCCT 60	CGAAAGAGAT	GAAGTATTT 3	TOCCAAA GCA	GAAAT CAGCA	ATCAAGTGGT	21
ACGGGAAATA 20	CCTCAACAAC	CCTCTTGGAC	GCATCATGAT	GTTAACCGTC	CAGTTTGTCC	22
rosastasoo cu	CTTGTACTTA	GCOTTTAACC	FOTOTGGGAG	AUCCTAT SAU	GGGTT030IT	**************************************
GOCATTICTT	JUCJAAUGUT	UCCATCTACA	AT BACCBAGA	ADGUDTODAG	APATALUTII	
CTGATGCGGG CC	TATTCTAGCC	GT CT GT TTTT 3	GT DTTTA DOG	TTACGCTGCT	GCACAAGGGA	24
TGGCCTCGAT	GATCTGCCTC	TAÇGGAGTAC	CGCTTCTGAT	AGTGAATGCG	TTOCTOGTOT	24

TGATCACTTA CT	TGCAGCAC	ACTCATCCCT	CGTTGCCTCA	CTACGATTCA	TCAGAGTGGG	25		
ACTGGCTCAG GG	GAGCTTTG	GCTACCGTAG	ACAGAGACTA	CGGAATCTTG	AACAAGGTGT	25		
TCCACAACAT TA 40	ACAGACACA	CACGTGGCTC	ATCACCTGTT	CTCGACAATG	CCGCATTATA	.26		
ACGCAATGGA AG	GCTACAAAG	GCGATAAAGC	CAATTCTGGG	AGACTATTAC	CAG'TTCGA'TG	27		
GAACACCGTG GT 60	TATGTGGCG	ATGTATAGGG	AGGCAAAGGA	GTGTATCTAT	GTAGAACCGG	27		
ACAGGGAAGG TG	SACAAGAAA	GGTGTGTACT	GGTACAACAA	TAAGTTATGA	GGATGATGGT	.:8		
GAAGAAATTG TC 80	CGACTTTTC	TCTTGTCTGT	TTGTCTTTTG	TTAAAGAAGC	TATGCTTCGT	28		
TTTAATAATC TT	PATTGTCCA	TTTTGTTGTG	TTATGACATT	TTGGCTGCTC	ATTATGTTAT	.19		
GTGGGAAGTT AG	GCGTTCAAA	TGTTTTGGCT	CGG			29		
(2) INFORMATION FOR SEQ ID NO:16:								
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STEANDEDNESS: single(D) TOPOLOGY: linear								
(ii)	MOLECU	LE TYPE: o	DNA					
(iii)	нувотн	ETICAL: NO)					
(vi)	AMTI-\$	ENSE: NO						
(ix) FEATURE: (A) NAME MEY: misc feature (B) LOCATION: 123 (A) COTHER INFORMATION: /croduct= "syntaging: (b) isoppolythis:"								
(xi)	នកខ្លះកង្គ	CE DESCRIPI	rion: SEQ 1	ID No:16:				
GUSCATGING AF	RAANAF.ETG	PT G		23				
(2) INFOR	RMATION FO	R SEQ ID NO	0:17:					
i :	SEQUEN	CE THARACTE	SPISTIUS:					

- (A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /product=
- "synthetic
- oligonuclectide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGCATGTRC TRAANAERTG ETG

23